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2858	80049806 (11691, 11692)	Novel Protein sim. GBank gil3122879 sp O07438 SYA_MYCTU - ALANYL- TRNA SYNTHETASE (ALANINE--TRNA LIGASE) (ALARS)	Contains protein domain (PF01411) - tRNA synthetases class II (A)	UNCLASSIFIED	1004, 1010, 1012, 1016, 1034, 1039, 1044
2859	80022287 (16637, 16638)	Novel Protein sim. GBank gil3122886 sp O34526 SYA_BACSU - ALANYL- TRNA SYNTHETASE (ALANINE--TRNA LIGASE) (ALARS)	Contains protein domain (PF01411) - tRNA synthetases class II (A)	UNCLASSIFIED	1004
2860	86473928 (11009, 11010)	Novel Protein sim. GBank gil419757 pir S30145 - ketol-acid reductoisomerase (EC 1.1.1.86) precursor - Arabidopsis thaliana	Contains protein domain (PF01450) - Acetohydroxy acid isomeroreductase	UNCLASSIFIED	1003, 1008, 1053, 1054
2861	79835057 (12141, 12142)	Novel Protein sim. GBank gil4204413 (AF047001) - Lys44 [Oenococcus oeni temperate bacteriophage fOg44]	Contains protein domain (PF01476) - Putative peptidoglycan binding domain	UNCLASSIFIED	1039
2862	20438269 (11797, 11798)	Novel Protein sim. GBank gil728840 sp P39046 ALYS_ENTHR - AUTOLYSIN PRECURSOR (N- ACETYLMURAMOYL-L-ALANINE AMIDASE) (MURAMIDASE-2)	Contains protein domain (PF01476) - Putative peptidoglycan binding domain	UNCLASSIFIED	1010
2863	86684852 (11347, 11348)	Novel Protein sim. GBank gil2326738 emb CAB10952] - (Z98268) hypothetical protein Rv1695 [Mycobacterium tuberculosis]	Contains protein domain (PF01513) - Domain of unknown function	UNCLASSIFIED	1001, 1004, 1006, 1008, 1010, 1012, 1018, 1019, 1022, 1024, 1025, 1026, 1027, 1029, 1030, 1031, 1034, 1038, 1039, 1053, 1054
2864	17938848 (11943, 11944)	Novel Protein sim. GBank gil154916 (M95402) - transposase [Transposon Tn5393]	Contains protein domain (PF01526) - Transposase	UNCLASSIFIED	1039
2865	57292642 (11273, 11274)	Novel Protein sim. GBank gil1176580 sp P42836 YN66_YEAST - HYPOTHETICAL 39.2 KD PROTEIN IN EGT2- KRE1 INTERGENIC REGION	Contains protein domain (PF01529) - DHHC zinc finger domain	UNCLASSIFIED	1004, 1006, 1017, 1022, 1024, 1034

2866	80430268 (5135, 5136)	Novel Protein sim. GBank gi 1666161 emb CAB03772 - (Z81451) hypothetical protein Rv2424c [Mycobacterium tuberculosis]	Contains protein domain (PF01548) - Transposase	UNCLASSIFIED	1026, 1038, 1044
2867	78673180 (9287, 9288)	Novel Protein sim. GBank gi 4980710 gb AAD35304.1 AE00170 - (AE001706) glycine cleavage system H protein [Thermotoga maritima]	Contains protein domain (PF01597) - Glycine cleavage H-protein	UNCLASSIFIED	1026, 1039
2868	87139316 (977, 978)	Novel Protein sim. GBank gi 3452358 (AF075724) - legiolsin [Legionella pneumophila]	Contains protein domain (PF01626) - 4- hydroxyphenylpyruvate dioxygenase C terminal domain	UNCLASSIFIED	1010
2869	85801185 (17125, 17126)	Novel Protein sim. GBank gi 3452358 (AF075724) - legiolsin [Legionella pneumophila]	Contains protein domain (PF01626) - 4- hydroxyphenylpyruvate dioxygenase C terminal domain	UNCLASSIFIED	1025
2870	20726398 (7365, 7366)	Novel Protein sim. GBank gi 729312 sp P07651 DEOB_ECOLI - PHOSPHOPENTOMUTASE (PHOSPHODEOXYRIBOMUTASE)	Contains protein domain (PF01676) - Metalloenzyme superfamily	UNCLASSIFIED	1006
2871	82060992 (10487, 10488)	Novel Protein sim. GBank gi 2498781 sp Q03674 PLB2_YEAST - PUTATIVE LYSOPHOSPHOLIPASE PRECURSOR (PHOSPHOLIPASE B)	Contains protein domain (PF01735) - Lysophospholipase catalytic domain	UNCLASSIFIED	1000, 1001, 1003, 1004, 1006, 1008, 1009, 1012, 1016, 1022, 1023, 1024, 1025, 1026, 1034, 1039, 1044
2872	78041806 (11655, 11656)	Novel Protein sim. GBank gi 2293162 (AF008220) - putative peptidase [Bacillus subtilis]	Contains protein domain (PF01738) - Dienelactone hydrolase family	UNCLASSIFIED	1044
2873	78484530 (2565, 2566)	Novel Protein sim. GBank gi 2833223 sp Q12460 SIK1_YEAST - SIK1 PROTEIN	Contains protein domain (PF01798) - Putative snoRNA binding domain	UNCLASSIFIED	1009

2874	81590727 (20343, 20344)	Novel Protein sim. GBank gij2739100 (AF027507) - primase [Mycobacterium smegmatis]	Contains protein domain (PF01807) - CHC2 zinc finger	UNCLASSIFIED	1054
2875	65452252 (5305, 5306)	Novel Protein sim. GBank gij202857 (M77183) - alpha-1-macroglobulin [Rattus norvegicus]	Contains protein domain (PF01835) - Alpha-2-macroglobulin family N-terminal region	UNCLASSIFIED	1016, 1044
2876	11767889 (10623, 10624)	Novel Protein sim. GBank gij1731343sp Q10694 YY25_MYCTU - HYPOTHETICAL 24.4 KD PROTEIN CY49.25	Contains protein domain (PF01836) - Transposase	UNCLASSIFIED	1022
2877	86885644 (18489, 18490)	Novel Protein sim. GBank gij95567 pir S21562 - hypothetical protein B - Erwinia amylovora	Contains protein domain (PF01836) - Transposase	UNCLASSIFIED	1029
2878	17960637 (21695, 21696)	Novel Protein sim. GBank gij1460074 emb CAB01049 - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis]	Contains protein domain (PF01841) - Transglutaminase-like superfamily	UNCLASSIFIED	1016
2879	80258641 (18249, 18250)	Novel Protein sim. GBank gij1518779 (U62581) - phenylalanine hydroxylase gene cluster transcription activator PhhR [Pseudomonas aeruginosa]	Contains protein domain (PF01842) - ACT domain	UNCLASSIFIED	1034
2880	78465452 (11555, 11556)	Novel Protein sim. GBank gij188864 (M74027) - mucin [Homo sapiens]	Contains protein domain (PF01844) - HNH endonuclease	UNCLASSIFIED	1003
2881	13883832 (15093, 15094)	Novel Protein sim. GBank gij2314032 gb AAD07943.1 - (AE000599) outer membrane protein (omp19) [Helicobacter pylori 26695]	Contains protein domain (PF01856) - Outer membrane protein	UNCLASSIFIED	1053
2882	79827273 (21911, 21912)	Novel Protein sim. GBank gij3261828 emb CAB10925 - (Z98260) mrip [Mycobacterium tuberculosis]	Contains protein domain (PF01883) - Domain of unknown function	UNCLASSIFIED	1004, 1017, 1031, 1044, 1049

2883	80431264 (20381, 20382)	Novel Protein sim. GBank gil731436[sp]P40010[YEJ6_YEAST - HYPOTHETICAL GTP-BINDING PROTEIN IN PM140-PAC2 INTERGENIC REGION	Contains protein domain (PF01926) - GTPase of unknown function	UNCLASSIFIED	1001, 1003, 1004, 1006, 1010, 1012, 1017, 1022, 1023, 1024, 1026, 1034, 1036, 1038, 1044, 1054
2884	78052499 (2561, 2562)	Novel Protein sim. GBank gil1722972[sp]Q10634[Y036_MYCTU - HYPOTHETICAL 25.1 KD PROTEIN CY130.06	Contains protein domain (PF01939) - Protein of unknown function	UNCLASSIFIED	1026
2885	19882099 (14089, 14090)	Novel Protein sim. GBank gil3250916[emb]CAA07434] - (AJ007291) CAP1 [Rattus norvegicus]	Contains protein domain (PF01965) - ThiJ/Pfp family	UNCLASSIFIED	1022
2886	81183403 (21255, 21256)	Novel Protein sim. GBank gil2634068[emb]CAB13569] - (Z99112) similar to hypothetical proteins [Bacillus subtilis]	Contains protein domain (PF01966) - HD domain	UNCLASSIFIED	1004, 1022, 1054
2887	80230242 (19107, 19108)	Novel Protein sim. GBank gil1001236[dbj]BAA10477] - (D64003) hypothetical protein [Synechocystis sp.]		UNCLASSIFIED	1004, 1006, 1010, 1022, 1031
2888	20465177 (1757, 1758)	Novel Protein sim. GBank gil1001423[dbj]BAA10046] - (D63999) hypothetical protein [Synechocystis sp.]		UNCLASSIFIED	1010
2889	10880972 (12769, 12770)	Novel Protein sim. GBank gil1001642[dbj]BAA10373] - (D64002) dGTP - triphosphohydrolase [Synechocystis sp.]		UNCLASSIFIED	1038
2890	94684783 (1905, 1906)	Novel Protein sim. GBank gil1001663[dbj]BAA10397] - (D64002) rare lipoprotein A [Synechocystis sp.]		UNCLASSIFIED	1010, 1022
2891	52561021 (83, 84)	Novel Protein sim. GBank gil1001693[dbj]BAA10430] - (D64002) hypothetical protein [Synechocystis sp.]		UNCLASSIFIED	1017
2892	79427000 (16341, 16342)	Novel Protein sim. GBank gil1001693[dbj]BAA10430] - (D64002) hypothetical protein [Synechocystis sp.]		UNCLASSIFIED	1017

2893	65981968 (7597, 7598)	Novel Protein sim. GBank gj 1006608 dbj BAA10762 - (D64005) pyridoxal phosphate biosynthetic protein PdxA [Synecocystis sp.]	UNCLASSIFIED	1024
2894	10371303 (18035, 18036)	Novel Protein sim. GBank gj 102424 pir A41132 - collagen-related protein 1 precursor - Hydra magnipapillata	UNCLASSIFIED	1017
2895	27837744 (9015, 9016)	Novel Protein sim. GBank gj 102425 pir B41132 - collagen-related protein 2 - Hydra magnipapillata (fragment)	UNCLASSIFIED	1053
2896	78965883 (4683, 4684)	Novel Protein sim. GBank gj 102426 pir C41132 - collagen-related protein 3 precursor - Hydra magnipapillata	UNCLASSIFIED	1030, 1054
2897	80078979 (4711, 4712)	Novel Protein sim. GBank gj 104266 pir B38274 - Y-box protein 2 - African clawed frog	UNCLASSIFIED	1034
2898	20294734 (4227, 4228)	Novel Protein sim. GBank gj 1044963 bbs 169646 protamine [Monodonta turbinata, gonads, Peptide, 106 aa]	UNCLASSIFIED	1034
2899	27843855 (11649, 11650)	Novel Protein sim. GBank gj 1044963 bbs 169646 protamine [Monodonta turbinata, gonads, Peptide, 106 aa]	UNCLASSIFIED	1022
2900	80077428 (21831, 21832)	Novel Protein sim. GBank gj 1044963 bbs 169646 protamine [Monodonta turbinata, gonads, Peptide, 106 aa]	UNCLASSIFIED	1034
2901	78732189 (8961, 8962)	Novel Protein sim. GBank gj 1050466 emb CAA62931 - (X91821) dsdC [Escherichia coli]	UNCLASSIFIED	1008
2902	21433573 (16759, 16760)	Novel Protein sim. GBank gj 1055163 gb AA81132.1 - (U40029) Contains similarity to Pfam domain: PF01060 (Worm_family_2), Score=203.8, E-value=8.6e-58, N=1 [Caenorhabditis elegans]	UNCLASSIFIED	1024
2903	20728042 (5113, 5114)	Novel Protein sim. GBank gj 1060876 dbj BAA11236 - (D78168) EmrK [Escherichia coli]	UNCLASSIFIED	1006

2904	49613196 (8343, 8344)	Novel Protein sim. GBank gij106322 pir B34087 - hypothetical protein (L1H 3' region) - human		UNCLASSIFIED	1036
2905	65706415 (12013, 12014)	Novel Protein sim. GBank gij106322 pir B34087 - hypothetical protein (L1H 3' region) - human		UNCLASSIFIED	1038
2906	78373241 (19887, 19888)	Novel Protein sim. GBank gij106322 pir B34087 - hypothetical protein (L1H 3' region) - human		UNCLASSIFIED	1009
2907	27348989 (20517, 20518)	Novel Protein sim. GBank gij106322 pir B34087 - hypothetical protein (L1H 3' region) - human		UNCLASSIFIED	1026
2908	19484846 (21275, 21276)	Novel Protein sim. GBank gij106322 pir B34087 - hypothetical protein (L1H 3' region) - human		UNCLASSIFIED	1016
2909	20286419 (11423, 11424)	Novel Protein sim. GBank gij106323 pir A34087 - hypothetical protein (L1H 5' region) - human		UNCLASSIFIED	1022
2910	79632735 (8897, 8898)	Novel Protein sim. GBank gij1064791 dbj BAA11277] - (D78193) yydE [Bacillus subtilis]		UNCLASSIFIED	1023
2911	39518435 (7585, 7586)	Novel Protein sim. GBank gij1065941 (U40799) - F42C5.7 gene product [Caenorhabditis elegans]		UNCLASSIFIED	1024
2912	79179027 (13467, 13468)	Novel Protein sim. GBank gij1072841 pir S52856 - AraC-like protein - Azorhizobium caulinodans		UNCLASSIFIED	1027
2913	79761936 (2065, 2066)	Novel Protein sim. GBank gij1073072 pir C55543 - cmaU protein - Pseudomonas syringae pv. syringae		UNCLASSIFIED	1023
2914	13517991 (16239, 16240)	Novel Protein sim. GBank gij1073504 pir S47741 - hypothetical protein o323 - Escherichia coli		UNCLASSIFIED	1024
2915	10237747 (19955, 19956)	Novel Protein sim. GBank gij107422 pir B36298 - proline-rich protein PRB3S (cys) - human (fragment)		UNCLASSIFIED	1025

2916	80238540 (6547, 6548)	Novel Protein sim. GBank gjl1075835 pir S49455 - deoxyribose-phosphate aldolase (EC 4.1.2.4) - <i>Bacillus subtilis</i>		UNCLASSIFIED	1004, 1031, 1040
2917	35019572 (983, 984)	Novel Protein sim. GBank gjl1076205 pir S50754 - hypothetical protein WP6 - <i>Chlamydomonas eugametos</i>		UNCLASSIFIED	1016
2918	80046339 (1109, 1110)	Novel Protein sim. GBank gjl1076211 pir S50755 - hypothetical protein VSP-3 - <i>Chlamydomonas reinhardtii</i>		UNCLASSIFIED	1023, 1024
2919	94139904 (3523, 3524)	Novel Protein sim. GBank gjl1076211 pir S50755 - hypothetical protein VSP-3 - <i>Chlamydomonas reinhardtii</i>		UNCLASSIFIED	1001, 1003, 1004, 1010, 1022, 1023, 1024, 1034
2920	47654638 (14149, 14150)	Novel Protein sim. GBank gjl1076211 pir S50755 - hypothetical protein VSP-3 - <i>Chlamydomonas reinhardtii</i>		UNCLASSIFIED	1029
2921	80497394 (18175, 18176)	Novel Protein sim. GBank gjl1076211 pir S50755 - hypothetical protein VSP-3 - <i>Chlamydomonas reinhardtii</i>		UNCLASSIFIED	1012
2922	23291231 (22479, 22480)	Novel Protein sim. GBank gjl1076211 pir S50755 - hypothetical protein VSP-3 - <i>Chlamydomonas reinhardtii</i>		UNCLASSIFIED	1003
2923	82384772 (1849, 1850)	Novel Protein sim. GBank gjl1077044 pir S53485 - carnitine O-acetyltransferase (EC 2.3.1.7), mitochondrial - yeast (<i>Saccharomyces cerevisiae</i>)		UNCLASSIFIED	1001, 1003, 1004, 1006, 1008, 1009, 1010, 1012, 1017, 1022, 1023, 1024, 1026, 1027, 1031, 1034, 1038, 1039, 1044, 1054

2924	88094563 (3765, 3766)	Novel Protein sim. GBank gij1077044 pir S53485 - carnitine O-acetyltransferase (EC 2.3.1.7), mitochondrial - yeast (<i>Saccharomyces cerevisiae</i>)		UNCLASSIFIED	1001, 1003, 1004, 1006, 1008, 1009, 1010, 1012, 1017, 1022, 1023, 1024, 1025, 1026, 1027, 1029, 1031, 1034, 1039, 1044, 1054
2925	28996027 (3373, 3374)	Novel Protein sim. GBank gij1077164 pir S52500 - SWH1 protein homolog YDL019c - yeast (<i>Saccharomyces cerevisiae</i>)		UNCLASSIFIED	1044
2926	78673811 (1701, 1702)	Novel Protein sim. GBank gij1077187 pir S49777 - probable membrane protein YDR180w - yeast (<i>Saccharomyces cerevisiae</i>)		UNCLASSIFIED	1026
2927	30672500 (871, 872)	Novel Protein sim. GBank gij1077350 pir S50381 - probable membrane protein YLR297w - yeast (<i>Saccharomyces cerevisiae</i>)		UNCLASSIFIED	1008
2928	79842541 (4119, 4120)	Novel Protein sim. GBank gij1077351 pir S50380 - probable membrane protein YLR296w - yeast (<i>Saccharomyces cerevisiae</i>)		UNCLASSIFIED	1008, 1022, 1024
2929	29684825 (1861, 1862)	Novel Protein sim. GBank gij1077356 pir S51378 - probable membrane protein YLR360w - yeast (<i>Saccharomyces cerevisiae</i>)		UNCLASSIFIED	1009
2930	80236763 (6389, 6390)	Novel Protein sim. GBank gij1077393 pir S51403 - probable membrane protein YLR266c - yeast (<i>Saccharomyces cerevisiae</i>)		UNCLASSIFIED	1009, 1010, 1017, 1024, 1025, 1044

2931	79763668 (5905, 5906)	Novel Protein sim. GBank gij1077404 pir S51422 - probable membrane protein YLR177w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1023
2932	84453120 (4749, 4750)	Novel Protein sim. GBank gij1077407 pir S51435 - hypothetical protein YLR190w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1004, 1006, 1008, 1010, 1012, 1022, 1024, 1029, 1034, 1038, 1049
2933	80245522 (16821, 16822)	Novel Protein sim. GBank gij1077408 pir S51424 - hypothetical protein YLR179c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1004, 1006, 1044
2934	27365573 (2485, 2486)	Novel Protein sim. GBank gij1077412 pir S51432 - hypothetical protein YLR187w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003, 1017, 1044
2935	29360701 (8009, 8010)	Novel Protein sim. GBank gij1077523 pir S51252 - probable membrane protein YDR101c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1009
2936	79242196 (15781, 15782)	Novel Protein sim. GBank gij1077539 pir S52698 - hypothetical protein YDR190c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003, 1017, 1044
2937	80222249 (22589, 22590)	Novel Protein sim. GBank gij1077575 pir S52682 - hypothetical protein YDR117c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003, 1004, 1010, 1024, 1044
2938	17895052 (7195, 7196)	Novel Protein sim. GBank gij1078074 pir S53405 - probable membrane protein YLR328w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1039
2939	79111065 (267, 268)	Novel Protein sim. GBank gij1078086 pir S53412 - probable membrane protein YLR425w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003, 1017
2940	21147788 (11029, 11030)	Novel Protein sim. GBank gij1082211 pir A55575 - ankyrin 3, long form - human		UNCLASSIFIED	1058

2941	19533783 (20697, 20698)	Novel Protein sim. GBank gi 1082604 pir S53363 - mucin 5AC (clone JER58) - human (fragment)	UNCLASSIFIED	1025
2942	36998752 (19063, 19064)	Novel Protein sim. GBank gi 1083739 pir A55163 - nucleolar protein Nopp140, hepatic - rat	UNCLASSIFIED	1001
2943	28393356 (21781, 21782)	Novel Protein sim. GBank gi 1083764 pir B48013 - proline-rich proteoglycan 2 precursor, parotid - rat	UNCLASSIFIED	1017
2944	87113894 (5821, 5822)	Novel Protein sim. GBank gi 1084141 pir JX0360 - Na+/H+ antiporter NhaA - Vibrio parahaemolyticus	UNCLASSIFIED	1048
2945	79573623 (11197, 11198)	Novel Protein sim. GBank gi 1084141 pir JX0360 - Na+/H+ antiporter NhaA - Vibrio parahaemolyticus	UNCLASSIFIED	1001
2946	20715380 (1303, 1304)	Novel Protein sim. GBank gi 1084649 pir S55965 - probable membrane protein YLR409c - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1022
2947	80234823 (13763, 13764)	Novel Protein sim. GBank gi 1084649 pir S55965 - probable membrane protein YLR409c - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1004, 1008, 1038
2948	80230802 (9219, 9220)	Novel Protein sim. GBank gi 1084783 pir S54079 - BRR1 protein - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1001, 1009, 1024, 1039
2949	79876174 (12467, 12468)	Novel Protein sim. GBank gi 1109750 emb CAA90900 - (Z54195) TieB protein [Escherichia coli]	UNCLASSIFIED	1017
2950	79623784 (15229, 15230)	Novel Protein sim. GBank gi 1110587 bbs 170532 (S79410) nuclear localization signals (NLS)-binding protein=spot-1 [mice, Balb/c, testes, Peptide, 140 aa] [Mus sp.]	UNCLASSIFIED	1022, 1023
2951	65882631 (3067, 3068)	Novel Protein sim. GBank gi 111816 pir S21348 - probable polypolyprotein-related protein 4 - rat	UNCLASSIFIED	1054

2952	29909721 (14623, 14624)	Novel Protein sim. GBank gij111816 pir S21348 - probable pol polyprotein-related protein 4 - rat		UNCLASSIFIED	1030
2953	90995101 (6373, 6374)	Novel Protein sim. GBank gij1123052 (U41994) - similar to glycoproteins [Caenorhabditis elegans]		UNCLASSIFIED	1009, 1010, 1020, 1026, 1034, 1038, 1039
2954	12694385 (5565, 5566)	Novel Protein sim. GBank gij112785 sp P05100 3MG1_ECOLI - DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I)		UNCLASSIFIED	1031
2955	79245890 (22769, 22770)	Novel Protein sim. GBank gij113158 sp P25516 ACO1_ECOLI - ACONITATE HYDRATASE 1 (CITRATE HYDROLYASE 1) (ACONITASE 1)		UNCLASSIFIED	1039
2956	21433552 (12805, 12806)	Novel Protein sim. GBank gij1136392 dbj BAA11482 - (D79987) similar to Schizosaccharomyces pombe cut1 + protein which regulates spindle pole body duplication. [Homo sapiens]		UNCLASSIFIED	1022
2957	14973768 (10539, 10540)	Novel Protein sim. GBank gij113641 sp P10177 ALKH_ECOLI - 4-HYDROXY-2-OXOGLUTARATE ALDOLASE (2-KETO-4-HYDROXYGLUTARATE ALDOLASE) (KHG-ALDOLASE) / 2-DEHYDRO-3-DEOXYPHOSPHOGLUCONATE ALDOLASE (PHOSPHO-2-DEHYDRO-3-DEOXYGLUCONATE ALDOLASE) (PHOSPHO-2-KETO-3-DEOXYGLUCONATE ALDOLASE) (...)		UNCLASSIFIED	1024
2958	78439509 (11151, 11152)	Novel Protein sim. GBank gij113666 sp P23959 ALUA_HUMAN - IIII ALU CLASS A WARNING ENTRY IIII		UNCLASSIFIED	1008
2959	27367421 (16137, 16138)	Novel Protein sim. GBank gij113666 sp P23959 ALUA_HUMAN - IIII ALU CLASS A WARNING ENTRY IIII		UNCLASSIFIED	1026

2960	27980277 (21435, 21436)	Novel Protein sim. GBank gil113666 sp P23959 ALUA_HUMAN - ALU CLASS A WARNING ENTRY		UNCLASSIFIED	1022
2961	55174715 (22017, 22018)	Novel Protein sim. GBank gil113666 sp P23959 ALUA_HUMAN - ALU CLASS A WARNING ENTRY		UNCLASSIFIED	1026
2962	90933051 (12747, 12748)	Novel Protein sim. GBank gil113667 sp P23960 ALUB_HUMAN - ALU CLASS B WARNING ENTRY		UNCLASSIFIED	1049
2963	49604227 (2589, 2590)	Novel Protein sim. GBank gil113668 sp P23961 ALUC_HUMAN - ALU CLASS C WARNING ENTRY		UNCLASSIFIED	1036
2964	78792083 (9973, 9974)	Novel Protein sim. GBank gil113668 sp P23961 ALUC_HUMAN - ALU CLASS C WARNING ENTRY		UNCLASSIFIED	1017
2965	91236588 (11641, 11642)	Novel Protein sim. GBank gil113668 sp P23961 ALUC_HUMAN - ALU CLASS C WARNING ENTRY		UNCLASSIFIED	1045
2966	32440873 (11811, 11812)	Novel Protein sim. GBank gil113668 sp P23961 ALUC_HUMAN - ALU CLASS C WARNING ENTRY		UNCLASSIFIED	1000
2967	78377465 (12265, 12266)	Novel Protein sim. GBank gil113668 sp P23961 ALUC_HUMAN - ALU CLASS C WARNING ENTRY		UNCLASSIFIED	1016, 1044
2968	65471910 (18537, 18538)	Novel Protein sim. GBank gil113668 sp P23961 ALUC_HUMAN - ALU CLASS C WARNING ENTRY		UNCLASSIFIED	1054
2969	79257936 (22457, 22458)	Novel Protein sim. GBank gil113668 sp P23961 ALUC_HUMAN - ALU CLASS C WARNING ENTRY		UNCLASSIFIED	1003
2970	71777223 (9441, 9442)	Novel Protein sim. GBank gil113671 sp P23964 ALUF_HUMAN - ALU CLASS F WARNING ENTRY		UNCLASSIFIED	1024, 1039
2971	10886338 (16999, 17000)	Novel Protein sim. GBank gil114009 sp P05636 APAG_ECOLI - APAG PROTEIN		UNCLASSIFIED	1027

2972	79617144 (2693, 2694)	Novel Protein sim. GBank gi 114073 sp P07672 APT_ECOLI - ADENINE PHOSPHORIBOSYLTRANSFERASE (APRT)		UNCLASSIFIED	1034
2973	20715326 (21353, 21354)	Novel Protein sim. GBank gi 114157 sp P22675 ARLY_CHLRE - ARGININOSUCCINATE LYASE (ARGINOSUCCINASE) (ASAL)		UNCLASSIFIED	1022
2974	78765614 (9833, 9834)	Novel Protein sim. GBank gi 1143538 emb CAA61138 - (X87883) mitochondrial capsule selenoprotein [Rattus norvegicus]		UNCLASSIFIED	1023, 1039
2975	80058750 (12813, 12814)	Novel Protein sim. GBank gi 1146192 (L47838) - putative [Bacillus subtilis]		UNCLASSIFIED	1010
2976	79568002 (7401, 7402)	Novel Protein sim. GBank gi 114878 sp P11435 BCPA_STRHY - CARBOXYVINYL-CARBOXYPHOSPHONATE PHOSPHORYLMUTASE (CARBOXYPHOSPHONOENOLPYRUVATE PHOSPHONOMUTASE) (CPEP PHOSPHONOMUTASE)		UNCLASSIFIED	1044
2977	94669043 (20705, 20706)	Novel Protein sim. GBank gi 1150834 (U42471) - Wiscott-Aldrich Syndrome protein homolog [Mus musculus]		UNCLASSIFIED	1022, 1024
2978	17884620 (17465, 17466)	Novel Protein sim. GBank gi 115160 sp P26762 BVGS_BORBR - VIRULENCE SENSOR PROTEIN BVGS PRECURSOR		UNCLASSIFIED	1039
2979	9856934 (7951, 7952)	Novel Protein sim. GBank gi 115284 sp CA12_BOVIN_1 - [Segment 1 of 2] COLLAGEN ALPHA 1(I) CHAIN		UNCLASSIFIED	1008
2980	13517921 (5119, 5120)	Novel Protein sim. GBank gi 1155068 emb CAA64425 - (X94976) cell wall- plasma membrane linker protein [Brassica napus]		UNCLASSIFIED	1024
2981	80026320 (5637, 5638)	Novel Protein sim. GBank gi 115953 sp P25342 CC10_YEAST - CELL DIVISION CONTROL PROTEIN 10		UNCLASSIFIED	1004

2982	20281932 (10945, 10946)	Novel Protein sim. GBank gi 1160355 (U33058) - UNC-89 [Caenorhabditis elegans]		UNCLASSIFIED	1022
2983	80254017 (4609, 4610)	Novel Protein sim. GBank gi 1166450 emb CAA64559 - (X95262) Tfm5 [Lycopersicon esculentum]		UNCLASSIFIED	1004, 1006, 1008, 1016, 1017, 1023, 1024
2984	78675362 (20027, 20028)	Novel Protein sim. GBank gi 116701 sp P05481 HEAD_BPPH8 - MAJOR HEAD PROTEIN (GPE) (GP5) (MAJOR COAT PROTEIN)		UNCLASSIFIED	1008
2985	10147068 (8803, 8804)	Novel Protein sim. GBank gi 1167955 (U43497) - putative 32.7 kDa jasmonate-induced protein [Hordeum vulgare]		UNCLASSIFIED	1054
2986	12840694 (11339, 11340)	Novel Protein sim. GBank gi 1168224 sp P44569 5NTD_HAEIN - PROBABLE 5'-NUCLEOTIDASE PRECURSOR		UNCLASSIFIED	1022
2987	66149064 (8003, 8004)	Novel Protein sim. GBank gi 1168373 sp P46815 AG84_MYCLE - ANTIGEN 84		UNCLASSIFIED	1003
2988	29459741 (8699, 8700)	Novel Protein sim. GBank gi 1168816 sp P30665 CC54_YEAST - CELL DIVISION CONTROL PROTEIN 54		UNCLASSIFIED	1026
2989	78747885 (16909, 16910)	Novel Protein sim. GBank gi 1169207 sp P21705 DA82_YEAST - DAL82 PROTEIN		UNCLASSIFIED	1022
2990	13086022 (2419, 2420)	Novel Protein sim. GBank gi 1169224 sp P44514 DAPE_HAEIN - SUCCINYL DIAMINOPIMELATE DESUCCINYLASE (SDAP)		UNCLASSIFIED	1022
2991	20438284 (14597, 14598)	Novel Protein sim. GBank gi 1169268 sp P44430 DEOC_HAEIN - DEOXYRIBOSE-PHOSPHATE ALDOLASE (PHOSPHODEOXYRIBOALDOLASE) (DEOXYRIBOALDOLASE)		UNCLASSIFIED	1010
2992	20466524 (9123, 9124)	Novel Protein sim. GBank gi 1169479 sp P43925 IEFG_HAEIN - ELONGATION FACTOR G (EF-G)		UNCLASSIFIED	1010

2993	19858781 (3139, 3140)	Novel Protein sim. GBank gil1169692 sp P41813 FKH2_YEAST - FORK HEAD PROTEIN HOMOLOG 2		UNCLASSIFIED	1022
2994	79618456 (21515, 21516)	Novel Protein sim. GBank gil1169692 sp P41813 FKH2_YEAST - FORK HEAD PROTEIN HOMOLOG 2		UNCLASSIFIED	1006
2995	35365320 (17355, 17356)	Novel Protein sim. GBank gil1169748 sp P43500 FRZC_MYXXA - FRZCD PROTEIN (FRIZZY AGGREGATION PROTEIN FRZCD)		UNCLASSIFIED	1050
2996	11083699 (12243, 12244)	Novel Protein sim. GBank gil1169821 sp P13227 GAL1_STRLI - GALACTOKINASE		UNCLASSIFIED	1024
2997	11688227 (15077, 15078)	Novel Protein sim. GBank gil1170243 sp P43413 HEMZ_YEREN - FERROCHELATASE (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE)		UNCLASSIFIED	1006
2998	20465707 (12665, 12666)	Novel Protein sim. GBank gil1170440 sp P44523 HXC1_HAEIN - HEME- HEMOPEXIN UTILIZATION PROTEIN C PRECURSOR		UNCLASSIFIED	1010
2999	30251531 (12613, 12614)	Novel Protein sim. GBank gil1170490 sp P46958 IDS2_YEAST - IME2- DEPENDENT SIGNALING PROTEIN		UNCLASSIFIED	1026
3000	21424644 (19235, 19236)	Novel Protein sim. GBank gil1170490 sp P46958 IDS2_YEAST - IME2- DEPENDENT SIGNALING PROTEIN		UNCLASSIFIED	1022
3001	80249907 (18633, 18634)	Novel Protein sim. GBank gil1170500 sp P44323 IF2_HAEIN - TRANSLATION INITIATION FACTOR IF-2		UNCLASSIFIED	1022, 1024, 1034
3002	79840765 (5857, 5858)	Novel Protein sim. GBank gil1170546 sp P44851 ILVD_HAEIN - DIHYDROXY-ACID DEHYDRATASE (DAD)		UNCLASSIFIED	1017
3003	66151504 (669, 670)	Novel Protein sim. GBank gil1170593 sp P14542 JUTA_ECOLI - FERRIC AEROBACTIN RECEPTOR PRECURSOR (CLOACIN RECEPTOR)		UNCLASSIFIED	1024

3004	16838677 (17495, 17496)	Novel Protein sim. GBank gij1170923 sp P44566 MEPA_HAEIN - PENICILLIN-INSENSITIVE MUREIN ENDOPEPTIDASE PRECURSOR		UNCLASSIFIED	1039
3005	20724429 (15081, 15082)	Novel Protein sim. GBank gij1170933 sp P45331 METE_HAEIN - 5- METHYL TETRAHYDROPTEROYL TRIGLUTAMA TE-HOMOCYSTEINE METHYLTRANSFERASE (METHIONINE SYNTHASE, VITAMIN-B12 INDEPENDENT ISOZYME) (COBALAMIN- INDEPENDENT METHIONINE SYNTHASE)		UNCLASSIFIED	1006
3006	80219473 (5967, 5968)	Novel Protein sim. GBank gij1170950 sp P43638 MHP1_YEAST - MAP- HOMOLOGOUS PROTEIN 1		UNCLASSIFIED	1003, 1004, 1006, 1010, 1022, 1024, 1026, 1034
3007	80468156 (8967, 8968)	Novel Protein sim. GBank gij1171071 sp P45066 MURC_HAEIN - UDP-N- ACETYLMURAMATE--ALANINE LIGASE (UDP-N- ACETYLMURANOYL-L-ALANINE SYNTHETASE)		UNCLASSIFIED	1012
3008	11077849 (11309, 11310)	Novel Protein sim. GBank gij1172222 (U44834) - polyphosphate glucokinase [Mycobacterium tuberculosis]		UNCLASSIFIED	1024
3009	79961872 (13373, 13374)	Novel Protein sim. GBank gij1172541 sp P47190 PMT3_YEAST - DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 3		UNCLASSIFIED	1006, 1010, 1023, 1024, 1034
3010	16843342 (21013, 21014)	Novel Protein sim. GBank gij1172543 sp P42934 PMT6_YEAST - DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 6		UNCLASSIFIED	1023

3011	52388083 (2143, 2144)	Novel Protein sim. GBank gil1172548 sp P43010 PNTB_HAEIN - NAD(P) TRANSHYDROGENASE SUBUNIT BETA (PYRIDINE NUCLEOTIDE TRANSHYDROGENASE SUBUNIT BETA) (NICOTINAMIDE NUCLEOTIDE TRANSHYDROGENASE SUBUNIT BETA)		UNCLASSIFIED	1036
3012	80060010 (16911, 16912)	Novel Protein sim. GBank gil1172548 sp P43010 PNTB_HAEIN - NAD(P) TRANSHYDROGENASE SUBUNIT BETA (PYRIDINE NUCLEOTIDE TRANSHYDROGENASE SUBUNIT BETA) (NICOTINAMIDE NUCLEOTIDE TRANSHYDROGENASE SUBUNIT BETA)		UNCLASSIFIED	1008, 1010, 1034
3013	19641642 (2853, 2854)	Novel Protein sim. GBank gil1172617 sp P44647 PRIA_HAEIN - PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y)		UNCLASSIFIED	1004
3014	80502022 (14297, 14298)	Novel Protein sim. GBank gil1172803 sp P43123 QRI1_YEAST - HYPOTHETICAL 53.5 KD PROTEIN IN PHO2- POL3 INTERGENIC REGION		UNCLASSIFIED	1001, 1004, 1006, 1008, 1009, 1010, 1012, 1017, 1022, 1023, 1024, 1026, 1027, 1034, 1038, 1039, 1044
3015	38915945 (10801, 10802)	Novel Protein sim. GBank gil1174092 (U43360) - reverse transcriptase [Peromyscus maniculatus]		UNCLASSIFIED	1026
3016	65668295 (22243, 22244)	Novel Protein sim. GBank gil1174503 sp P43817 SYD_HAEIN - ASPARTYL- TRNA SYNTHETASE (ASPARTATE--TRNA LIGASE) (ASPRS)		UNCLASSIFIED	1016
3017	25260301 (4541, 4542)	Novel Protein sim. GBank gil1174549 sp P43834 SYV_HAEIN - VALYL- TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS)		UNCLASSIFIED	1008

3018	30503862 (705, 706)	Novel Protein sim. GBank gil1174661 sp P44594 TGT_HAEIN - QUEUEINE TRNA-RIBOSYLTRANSFERASE (TRNA- GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)		UNCLASSIFIED	1009
3019	78795379 (3317, 3318)	Novel Protein sim. GBank gil1174933 sp P44907 VACB_HAEIN - VACB PROTEIN HOMOLOG		UNCLASSIFIED	1026
3020	78757424 (9923, 9924)	Novel Protein sim. GBank gil1174933 sp P44907 VACB_HAEIN - VACB PROTEIN HOMOLOG		UNCLASSIFIED	1030
3021	17902237 (16721, 16722)	Novel Protein sim. GBank gil1175115 sp P41479 Y091_NPVAC - HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION		UNCLASSIFIED	1044
3022	11070511 (18511, 18512)	Novel Protein sim. GBank gil1175173 sp P43954 Y152_HAEIN - HYPOTHETICAL PROTEIN HI0152		UNCLASSIFIED	1006
3023	20436657 (15399, 15400)	Novel Protein sim. GBank gil1175322 sp P44917 Y883_HAEIN - HYPOTHETICAL PROTEIN HI0883		UNCLASSIFIED	1010
3024	80221613 (7483, 7484)	Novel Protein sim. GBank gil1175395 sp Q09723 YA42_SCHPO - HYPOTHETICAL 14.1 KD PROTEIN C31A2.02 IN CHROMOSOME I		UNCLASSIFIED	1004, 1006, 1010, 1022, 1024, 1026, 1034
3025	11093343 (4863, 4864)	Novel Protein sim. GBank gil1175512 sp P39717 YAF6_YEAST - HYPOTHETICAL 95.1 KD PROTEIN IN CNE1- ACS1 INTERGENIC REGION		UNCLASSIFIED	1022
3026	16425308 (8001, 8002)	Novel Protein sim. GBank gil1175641 sp P44720 YCEG_HAEIN - HYPOTHETICAL PROTEIN HI0457		UNCLASSIFIED	1017
3027	78917082 (22569, 22570)	Novel Protein sim. GBank gil1175652 sp P44551 TRMU_HAEIN - PROBABLE TRNA (5-METHYLAMINOMETHYL-2- THIOURIDYLATE)-METHYLTRANSFERASE		UNCLASSIFIED	1039

3028	27348644 (16079, 16080)	Novel Protein sim. GBank gil1175653 sp P44796 YFCF_HAEIN - HYPOTHETICAL PROTEIN HI0638	UNCLASSIFIED	1022
3029	20724165 (16651, 16652)	Novel Protein sim. GBank gil1175655 sp P44683 YCFD_HAEIN - HYPOTHETICAL PROTEIN HI0396	UNCLASSIFIED	1006
3030	85808835 (16085, 16086)	Novel Protein sim. GBank gil1175866 sp P44227 YF05_HAEIN - HYPOTHETICAL PROTEIN HI1505	UNCLASSIFIED	1001, 1031, 1038
3031	11608969 (3233, 3234)	Novel Protein sim. GBank gil1175927 sp P43578 YFB5_YEAST - HYPOTHETICAL 19.3 KD PROTEIN IN MDJ1- HSP12 INTERGENIC REGION	UNCLASSIFIED	1022
3032	80079333 (3815, 3816)	Novel Protein sim. GBank gil1175986 sp P43595 YFI2_YEAST - HYPOTHETICAL 22.4 KD PROTEIN IN GCN20- CMK1 INTERGENIC REGION PRECURSOR	UNCLASSIFIED	1006, 1017, 1034, 1039
3033	80546722 (12225, 12226)	Novel Protein sim. GBank gil1175990 sp P43598 YFI7_YEAST - HYPOTHETICAL 21.8 KD PROTEIN IN UGS1- FAB1 INTERGENIC REGION	UNCLASSIFIED	1001, 1004, 1006, 1008, 1010, 1022, 1023, 1024, 1027, 1031, 1034, 1058
3034	80503206 (14003, 14004)	Novel Protein sim. GBank gil1176023 sp P43618 YFL6_YEAST - HYPOTHETICAL 41.3 KD PROTEIN IN SAP155- YMR31 INTERGENIC REGION	UNCLASSIFIED	1001, 1003, 1004, 1006, 1012, 1017, 1022, 1024, 1034, 1044, 1054
3035	57293445 (7473, 7474)	Novel Protein sim. GBank gil1176026 sp P43621 COPD_YEAST - COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)	UNCLASSIFIED	1022, 1034
3036	87462658 (13775, 13776)	Novel Protein sim. GBank gil1176160 sp P42626 YHAM_ECOLI - HYPOTHETICAL 19.4 KD PROTEIN IN EXUR- TDCC INTERGENIC REGION (F188)	UNCLASSIFIED	1004, 1006, 1010, 1015, 1016, 1024

3037	77520579 (16077, 16078)	Novel Protein sim. GBank gil1176266[sp]P45804[YHGE_ECOLI - HYPOTHETICAL 64.6 KD PROTEIN IN MRCA- PCKA INTERGENIC REGION (F574)]		UNCLASSIFIED	1049
3038	79835018 (5813, 5814)	Novel Protein sim. GBank gil1176281[sp]P46852[YHHW_ECOLI - HYPOTHETICAL 26.3 KD PROTEIN IN GNTR- GGT INTERGENIC REGION (F231)]		UNCLASSIFIED	1008
3039	80412661 (6701, 6702)	Novel Protein sim. GBank gil1176481[sp]P39408[YJV_ECOLI - HYPOTHETICAL 28.9 KD PROTEIN IN OSMY- DEOC INTERGENIC REGION]		UNCLASSIFIED	1029
3040	78741833 (18065, 18066)	Novel Protein sim. GBank gil1176587[sp]P42843[YN51_YEAST - HYPOTHETICAL 88.9 KD PROTEIN IN RFA2- STB1 INTERGENIC REGION]		UNCLASSIFIED	1008
3041	82337545 (22717, 22718)	Novel Protein sim. GBank gil1176589[sp]P42845[STB1_YEAST - STB1 PROTEIN]		UNCLASSIFIED	1001, 1003, 1004, 1006, 1010, 1012, 1016, 1017, 1022, 1023, 1024, 1027, 1031, 1034, 1038, 1039, 1044
3042	35933693 (13009, 13010)	Novel Protein sim. GBank gil1176707[sp]P45637[YPRA_CORGL - HYPOTHETICAL 33.0 KD PROTEIN IN PROB- PROA INTERGENIC REGION]		UNCLASSIFIED	1053
3043	78675448 (521, 522)	Novel Protein sim. GBank gil1176918[sp]P24089[YSY2_YEAST - HYPOTHETICAL 137.7 KD PROTEIN IN SUBTELOMERIC Y' REPEAT REGION OF CHR XV (ORF 2)]		UNCLASSIFIED	1022
3044	25316869 (15795, 15796)	Novel Protein sim. GBank gil1176986[sp]P42413[IOLB_BACSU - IOLB PROTEIN]		UNCLASSIFIED	1008

3045	78786773 (5179, 5180)	Novel Protein sim. GBank gil117607 emb CAA63219 - (X92485) pva1 [Plasmodium vivax]		UNCLASSIFIED	1044
3046	20466944 (20991, 20992)	Novel Protein sim. GBank gil118244 sp P24176 DAPE_ECOLI - SUCCINYL- DIAMINOPIMELATE DESUCCINYLAASE (SDAP)		UNCLASSIFIED	1010
3047	20729206 (8609, 8610)	Novel Protein sim. GBank gil118248 sp P13483 DATI_YEAST - OLIGO(A)/OLIGO(T)-BINDING PROTEIN (DATIN)		UNCLASSIFIED	1010
3048	30001150 (8871, 8872)	Novel Protein sim. GBank gil118412 sp P09548 DEDA_ECOLI - DEDA PROTEIN (DSG-1 PROTEIN)		UNCLASSIFIED	1030
3049	12969395 (7621, 7622)	Novel Protein sim. GBank gil1184121 (U20808) - auxin-induced protein [Migna radiata]		UNCLASSIFIED	1024
3050	78789040 (10609, 10610)	Novel Protein sim. GBank gil119110 sp P03211 EBN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	1008
3051	32545225 (6651, 6652)	Novel Protein sim. GBank gil119111 sp P12978 EBN2_EBV - EBNA-2 NUCLEAR PROTEIN		UNCLASSIFIED	1023
3052	80248724 (16629, 16630)	Novel Protein sim. GBank gil1195494 bbs 170178 - Pax-1 product=sclerotome development regulator/DNA-binding transcriptional activator [Coturnix coturnix=Japanese quails, ssp. japonica, Peptide, 353 aa]		UNCLASSIFIED	1053
3053	80225738 (16205, 16206)	Novel Protein sim. GBank gil1196398 (M21305) - unknown protein [Homo sapiens]		UNCLASSIFIED	1053
3054	9282925 (7381, 7382)	Novel Protein sim. GBank gil1196743 (M14365) - unknown protein [Pseudomonas syringae]		UNCLASSIFIED	1003
3055	65681679 (19121, 19122)	Novel Protein sim. GBank gil119714 sp P13983 EXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE- RICH GLYCOPROTEIN)		UNCLASSIFIED	1046

3056	37811605 (22153, 22154)	Novel Protein sim. GBank gi 119928 sp P27787 FER1_MAIZE - FERREDOXIN I PRECURSOR (FD I)		UNCLASSIFIED	1058
3057	80430917 (22633, 22634)	Novel Protein sim. GBank gi 1199536 emb CAA64900 - (X95644) ORF 2310 [Saccharomyces cerevisiae]		UNCLASSIFIED	1006, 1038
3058	82101992 (15149, 15150)	Novel Protein sim. GBank gi 120304 sp P15932 FLGK_SALTY - FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 (HAP1)		UNCLASSIFIED	1016, 1024
3059	79628254 (12803, 12804)	Novel Protein sim. GBank gi 120393 sp P13421 FMA_SERMA - FIMBRIA A PROTEIN PRECURSOR		UNCLASSIFIED	1039
3060	79231403 (7845, 7846)	Novel Protein sim. GBank gi 121058 sp P12754 E2BD_YEAST - TRANSLATION INITIATION FACTOR EIF-2B DELTA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR) (GUANINE NUCLEOTIDE EXCHANGE FACTOR SUBUNIT GCD2) (GCD COMPLEX SUBUNIT GCD2)		UNCLASSIFIED	1001, 1017
3061	87896252 (687, 688)	Novel Protein sim. GBank gi 1213021 emb CAA59198 - (X84710) ORF492, surface antigen gene [Methanosarcina mazei]		UNCLASSIFIED	1015
3062	78949714 (7795, 7796)	Novel Protein sim. GBank gi 121644 sp P17816 GRP_HORVU - GLYCINE- RICH CELL WALL STRUCTURAL PROTEIN PRECURSOR		UNCLASSIFIED	1023
3063	85518675 (22333, 22334)	Novel Protein sim. GBank gi 121893 sp P13364 GYRB_PSEPU - DNA GYRASE SUBUNIT B		UNCLASSIFIED	1049
3064	70949771 (20929, 20930)	Novel Protein sim. GBank gi 123153 sp P16249 HIS5_STRCO - AMIDOTRANSFERASE HISH		UNCLASSIFIED	1029

3065	47666134 (17539, 17540)	Novel Protein sim. GBank gij1234787 (U37373) - up-regulated by thyroid hormone in tadpoles; expressed specifically in the tail and only at metamorphosis; membrane bound or extracellular protein; C-terminal basic region [Xenopus laevis]		UNCLASSIFIED	1040
3066	20375525 (6805, 6806)	Novel Protein sim. GBank gij123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	1010
3067	20717335 (20081, 20082)	Novel Protein sim. GBank gij123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	1034
3068	91213832 (13991, 13992)	Novel Protein sim. GBank gij1235974 emb CAA65474 - (X96713) collagen [Globodera pallida]		UNCLASSIFIED	1016, 1024
3069	15023758 (3185, 3186)	Novel Protein sim. GBank gij1236781 emb CAA65507 - (X96732) cuticular collagen [Osteria circumdata]		UNCLASSIFIED	1001
3070	80504151 (6465, 6466)	Novel Protein sim. GBank gij125329 sp P04951 KDSB_ECOLI - 3-DEOXY-MANNO-OCTULOSONATE CYTIDYLTRANSFERASE (CMP-KDO SYNTHETASE) (CMP-2-KETO-3-DEOXYOCTULOSONIC ACID SYNTHETASE) (CKS)		UNCLASSIFIED	1012
3071	11245720 (9245, 9246)	Novel Protein sim. GBank gij125963 sp P11048 LAMA_XENILA - LAMIN A		UNCLASSIFIED	1010
3072	57301013 (357, 358)	Novel Protein sim. GBank gij126215 sp P13838 LEUK_RAT - LEUKOSIALIN PRECURSOR (LEUCOCYTE SIALOGLYCOPROTEIN) (SIALOPHORIN) (CD43) (W3/13 ANTIGEN)		UNCLASSIFIED	1006, 1029, 1034, 1044
3073	28392794 (22241, 22242)	Novel Protein sim. GBank gij1262369 emb CAA94716 - (Z70722) hypothetical protein [Mycobacterium leprae]		UNCLASSIFIED	1044

3074	70942037 (12741, 12742)	Novel Protein sim. GBank gil126295 sp P08547 LIN1_HUMAN - LINE-1 REVERSE TRANSCRIPTASE HOMOLOG		UNCLASSIFIED	1024
3075	78462796 (13501, 13502)	Novel Protein sim. GBank gil126296 sp P08548 LIN1_NYCCO - LINE-1 REVERSE TRANSCRIPTASE HOMOLOG		UNCLASSIFIED	1026
3076	79247392 (1213, 1214)	Novel Protein sim. GBank gil126654 sp P03030 LYSR_ECOLI - TRANSCRIPTIONAL ACTIVATOR PROTEIN LYSR		UNCLASSIFIED	1039
3077	80021388 (12153, 12154)	Novel Protein sim. GBank gil126725 sp P21139 MAN1_RAT - ALPHA- MANNOSIDASE (ALPHA-D-MANNOSIDE MANNOHYDROLASE)		UNCLASSIFIED	1006, 1022
3078	82125916 (9133, 9134)	Novel Protein sim. GBank gil127028 sp P15807 MET8_YEAST - MET8 PROTEIN		UNCLASSIFIED	1004, 1006, 1012, 1016, 1022, 1024, 1025, 1026, 1034, 1039
3079	39713192 (19051, 19052)	Novel Protein sim. GBank gil127114 sp P23060 MK32_YEAST - MAK32 PROTEIN		UNCLASSIFIED	1026
3080	20212392 (17259, 17260)	Novel Protein sim. GBank gil1272368 (U51896) - LigE [Vibrio parahaemolyticus]		UNCLASSIFIED	1010
3081	82437397 (2193, 2194)	Novel Protein sim. GBank gil127550 sp P1653 MUTB_PROFR - METHYLMALONYL-COA MUTASE ALPHA- SUBUNIT (MCM-ALPHA)		UNCLASSIFIED	1001, 1004, 1010, 1012, 1022, 1027, 1034, 1038, 1049
3082	57300594 (19741, 19742)	Novel Protein sim. GBank gil1293563 (U49188) - Dif33 gene product [Homo sapiens]		UNCLASSIFIED	1010, 1022
3083	20608418 (1011, 1012)	Novel Protein sim. GBank gil129541 sp P15558 PAC2_PSES3 - PENICILLIN ACYLASE II PRECURSOR (PENICILLIN AMIDASE II) (CEPHALOSPORIN ACYLASE II)		UNCLASSIFIED	1004

3084	20724611 (14715, 14716)	Novel Protein sim. GBank gil129670 sp P02918 BPBA_ECOLI - PENICILLIN-BINDING PROTEIN 1A (PBP-1A)		UNCLASSIFIED	1006
3085	79607900 (20537, 20538)	Novel Protein sim. GBank gil129828 sp P24328 PERT_BORPA - PERTACTIN PRECURSOR (OUTER MEMBRANE PROTEIN P.70) (P.95)		UNCLASSIFIED	1034
3086	7892963 (13165, 13166)	Novel Protein sim. GBank gil130776 sp P20006 PPLA_RABIT - CARDIAC PHOSPHOLAMBAN (PLB)		UNCLASSIFIED	1008
3087	20292941 (3973, 3974)	Novel Protein sim. GBank gil130999 sp P05142 PRP2_MOUSE - PROLINE-RICH PROTEIN MP-2 PRECURSOR		UNCLASSIFIED	1034
3088	6757112 (8181, 8182)	Novel Protein sim. GBank gil131000 sp P10164 PRP2_RAT - ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25)		UNCLASSIFIED	1022
3089	80216614 (7201, 7202)	Novel Protein sim. GBank gil131002 sp P05143 PRP3_MOUSE - PROLINE-RICH PROTEIN MP-3		UNCLASSIFIED	1009, 1024, 1031
3090	20290873 (17893, 17894)	Novel Protein sim. GBank gil1314732 (U54640) - 185 kDa silk protein [Chironomus pallidivittatus]		UNCLASSIFIED	1034
3091	78758266 (18971, 18972)	Novel Protein sim. GBank gil131653 sp P25502 PUT3_YEAST - PROLINE UTILIZATION TRANS-ACTIVATOR		UNCLASSIFIED	1039, 1044, 1054
3092	57303110 (18523, 18524)	Novel Protein sim. GBank gil132339 sp P03872 REP2_YEAST - TRANS-ACTING FACTOR C (REP2) (PROTEIN CHARLIE)		UNCLASSIFIED	1004, 1022, 1026, 1034, 1039
3093	79568236 (5679, 5680)	Novel Protein sim. GBank gil132360 sp P05684 REPC_AGRRA - POSSIBLE REPLICATION PROTEIN C		UNCLASSIFIED	1008

3094	78755150 (3441, 3442)	Novel Protein sim. GBank gil132562 sp P25235 RIB2_RAT - DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE 63 KD SUBUNIT PRECURSOR (RIBOPHORIN II)	UNCLASSIFIED	1009
3095	36622940 (8273, 8274)	Novel Protein sim. GBank gil1326381 (U58751) - coded for by C. elegans cDNA yk9h5.5; coded for by C. elegans cDNA yk9h5.3; coded for by C. elegans cDNA CEESH72F; coded for by C. elegans cDNA CEESB62F; coded for by C. elegans cDNA yk110g2.3; coded for by C. elegans cDNA yk110g2.5...	UNCLASSIFIED	1034
3096	65657000 (9415, 9416)	Novel Protein sim. GBank gil1335199 emb CAA26919 - (X03145) pot. ORF V [Homo sapiens]	UNCLASSIFIED	1054
3097	10173056 (231, 232)	Novel Protein sim. GBank gil1335205 emb CAA36480 - (X52235) ORFII [Homo sapiens]	UNCLASSIFIED	1001
3098	33188734 (8665, 8666)	Novel Protein sim. GBank gil1335205 emb CAA36480 - (X52235) ORFII [Homo sapiens]	UNCLASSIFIED	1026
3099	80077692 (2217, 2218)	Novel Protein sim. GBank gil134319 sp P07819 SCRB_BACSU - SUCROSE-6-PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)	UNCLASSIFIED	1034
3100	37001319 (1769, 1770)	Novel Protein sim. GBank gil134398 sp P15040 SECB_ECOLI - PROTEIN-EXPORT PROTEIN SECB	UNCLASSIFIED	1001
3101	9883571 (14501, 14502)	Novel Protein sim. GBank gil134400 sp P16920 SECE_ECOLI - PREPROTEIN TRANSLOCASE SECE SUBUNIT	UNCLASSIFIED	1008
3102	17950910 (557, 558)	Novel Protein sim. GBank gil1346563 sp P49308 MOCB_RHIME - PUTATIVE RHIZOPINE-BINDING PROTEIN PRECURSOR	UNCLASSIFIED	1054

3103	78363353 (8369, 8370)	Novel Protein sim. GBank gil1346647 sp P49687 N145_YEAST - NUCLEOPORIN NUP145 (NUCLEAR PORE PROTEIN NUP145)		UNCLASSIFIED	1003
3104	11310751 (19601, 19602)	Novel Protein sim. GBank gil1346886 sp P25270 PT56_YEAST - RIBOSE METHYLTRANSFERASE PET56 (MITOCHONDRIAL LARGE RIBOSOMAL RNA RIBOSE METHYLASE) (21S RRNA [GM2251] 2'O METHYLTRANSFERASE)		UNCLASSIFIED	1022
3105	39432508 (19695, 19696)	Novel Protein sim. GBank gil1346886 sp P25270 PT56_YEAST - RIBOSE METHYLTRANSFERASE PET56 (MITOCHONDRIAL LARGE RIBOSOMAL RNA RIBOSE METHYLASE) (21S RRNA [GM2251] 2'O METHYLTRANSFERASE)		UNCLASSIFIED	1006
3106	80240870 (10127, 10128)	Novel Protein sim. GBank gil1346910 sp P28650 PUA1_MOUSE - ADENYLOSUCGINATE SYNTHETASE, MUSCLE ISOZYME (IMP-ASPARTATE LIGASE)		UNCLASSIFIED	1022
3107	79873033 (12885, 12886)	Novel Protein sim. GBank gil134752 sp P17122 SP16_YEAST - SPORULATION PROTEIN SPO16		UNCLASSIFIED	1001, 1006, 1022
3108	79910699 (16435, 16436)	Novel Protein sim. GBank gil134856 sp P09139 SPYA_RAT - SERINE-- PYRUVATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (SPT) (ALANINE--GLYOXYLATE AMINOTRANSFERASE) (AGT)		UNCLASSIFIED	1023
3109	27843819 (4371, 4372)	Novel Protein sim. GBank gil134920 sp P21997 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)		UNCLASSIFIED	1034

3110	11017734 (4395, 4396)	Novel Protein sim. GBank gil134920 sp P21997 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)		UNCLASSIFIED	1001
3111	80032445 (16297, 16298)	Novel Protein sim. GBank gil134935 sp P11972 SST2_YEAST - SST2 PROTEIN		UNCLASSIFIED	1001, 1004, 1006, 1008, 1022
3112	78789044 (11047, 11048)	Novel Protein sim. GBank gil1351823 sp P48238 YG30_YEAST - HYPOTHETICAL 25.2 KD PROTEIN IN RSR1-CYS4 INTERGENIC REGION		UNCLASSIFIED	1003, 1026
3113	78473387 (18227, 18228)	Novel Protein sim. GBank gil135192 sp P22326 SY1_BACSU - TYROSYL-TRNA SYNTHETASE 1 (TYROSINE--TRNA LIGASE) (TYRS 1)		UNCLASSIFIED	1026
3114	9274026 (15995, 15996)	Novel Protein sim. GBank gil1352123 sp P21637 COBG_PSEDE - COBG PROTEIN		UNCLASSIFIED	1004
3115	78916113 (4179, 4180)	Novel Protein sim. GBank gil1352209 sp P32325 DBF4_YEAST - DBF4 PROTEIN (DNA52 PROTEIN)		UNCLASSIFIED	1022, 1039
3116	80053089 (1671, 1672)	Novel Protein sim. GBank gil1352429 sp P02995 IF2_ECOLI - TRANSLATION INITIATION FACTOR IF-2		UNCLASSIFIED	1004
3117	78726661 (18631, 18632)	Novel Protein sim. GBank gil1352955 sp P47076 YJB1_YEAST - HYPOTHETICAL 18.6 KD PROTEIN IN CCT3-CCT8 INTERGENIC REGION		UNCLASSIFIED	1022, 1026
3118	57292988 (14891, 14892)	Novel Protein sim. GBank gil1352961 sp P47070 YJB8_YEAST - HYPOTHETICAL 11.7 KD PROTEIN IN PET130-CCT3 INTERGENIC REGION		UNCLASSIFIED	1004, 1006, 1010, 1024, 1034
3119	27848737 (17097, 17098)	Novel Protein sim. GBank gil1352966 sp P47063 YJC7_YEAST - HYPOTHETICAL 15.7 KD PROTEIN IN MAD2-RNR2 INTERGENIC REGION		UNCLASSIFIED	1022, 1024, 1034

3120	27366151 (9787, 9788)	Novel Protein sim. GBank gil1353033 sp P46993 YJR0_YEAST - HYPOTHETICAL 22.0 KD PROTEIN IN CPS1- FPP1 INTERGENIC REGION		UNCLASSIFIED	1022
3121	57302037 (21081, 21082)	Novel Protein sim. GBank gil1353033 sp P46993 YJR0_YEAST - HYPOTHETICAL 22.0 KD PROTEIN IN CPS1- FPP1 INTERGENIC REGION		UNCLASSIFIED	1008, 1034
3122	78938103 (10325, 10326)	Novel Protein sim. GBank gil1353046 sp P47082 YJX1_YEAST - HYPOTHETICAL 65.3 KD PROTEIN IN PRE3- SAG1 INTERGENIC REGION		UNCLASSIFIED	1017
3123	78948525 (22561, 22562)	Novel Protein sim. GBank gil1353108 sp P48566 YN33_YEAST - HYPOTHETICAL 73.0 KD PROTEIN IN CLA4- MID1 INTERGENIC REGION		UNCLASSIFIED	1017, 1022, 1023
3124	17294765 (1945, 1946)	Novel Protein sim. GBank gil1353221 sp P13390 VLTf_BPT5 - L-SHAPED TAIL FIBRE PROTEIN (LTF PROTEIN)		UNCLASSIFIED	1039
3125	16778371 (5223, 5224)	Novel Protein sim. GBank gil1353537 (U38906) - dUTPase [Bacteriophage r1t]		UNCLASSIFIED	1044
3126	79769235 (9779, 9780)	Novel Protein sim. GBank gil135514 sp P06333 TCB1_RABIT - T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11)		UNCLASSIFIED	1017
3127	80500474 (20245, 20246)	Novel Protein sim. GBank gil135700 sp P19675 TGT_ECOLI - QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA- GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)		UNCLASSIFIED	1012
3128	55007249 (21497, 21498)	Novel Protein sim. GBank gil135914 sp P17408 TLM_MOUSE - TLM PROTEIN (TLM ONCOGENE)		UNCLASSIFIED	1019
3129	78385457 (6405, 6406)	Novel Protein sim. GBank gil1361057 pir S56582 - hypothetical protein f192 - Escherichia coli		UNCLASSIFIED	1026

3130	85516635 (14423, 14424)	Novel Protein sim. GBank gi 1361153 pir S56602 - hypothetical protein o211 - Escherichia coli	UNCLASSIFIED	1049
3131	27981297 (15969, 15970)	Novel Protein sim. GBank gi 136141 sp P19774 TRA9_MYCTU - PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS986 (ORF8)	UNCLASSIFIED	1006
3132	11764353 (17809, 17810)	Novel Protein sim. GBank gi 136141 sp P19774 TRA9_MYCTU - PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS986 (ORF8)	UNCLASSIFIED	1022
3133	37034111 (21619, 21620)	Novel Protein sim. GBank gi 136141 sp P19774 TRA9_MYCTU - PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS986 (ORF8)	UNCLASSIFIED	1012
3134	24128986 (17695, 17696)	Novel Protein sim. GBank gi 1362491 pir S58652 - hypothetical protein YFR036w-a - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1009
3135	11356483 (22753, 22754)	Novel Protein sim. GBank gi 136250 sp P09880 TRNL_YEAST - TRNA LIGASE	UNCLASSIFIED	1058
3136	19883172 (12345, 12346)	Novel Protein sim. GBank gi 1363732 pir S59413 - probable membrane protein YLR454w - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1001
3137	57292361 (17991, 17992)	Novel Protein sim. GBank gi 1363762 pir S58825 - hypothetical protein YPR195c - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1004, 1006, 1010, 1022, 1024, 1027, 1034
3138	80308145 (13195, 13196)	Novel Protein sim. GBank gi 136482 sp P16649 TUP1_YEAST - GLUCOSE REPRESSION REGULATORY PROTEIN TUP1 (FLOCCULATION SUPPRESSOR PROTEIN) (REPRESSOR AER2)	UNCLASSIFIED	1006, 1025, 1029, 1039

3139	20480452 (7353, 7354)	Novel Protein sim. GBank gil136593 sp P04693 TYRB_ECOLI - AROMATIC-AMINO-ACID AMINOTRANSFERASE	UNCLASSIFIED	1034
3140	78492156 (12059, 12060)	Novel Protein sim. GBank gil136956 sp P16818 UL61_HCMVA - HYPOTHETICAL PROTEIN UL61	UNCLASSIFIED	1030
3141	80499918 (6251, 6252)	Novel Protein sim. GBank gil1370209 emb CAA66893 - (X98238) putative; orf1 [Lactobacillus sakei]	UNCLASSIFIED	1012
3142	24144522 (1983, 1984)	Novel Protein sim. GBank gil1399966 (U62317) - Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence [Homo sapiens]	UNCLASSIFIED	1053
3143	21432563 (2037, 2038)	Novel Protein sim. GBank gil1399966 (U62317) - Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence [Homo sapiens]	UNCLASSIFIED	1004, 1010
3144	39524559 (12919, 12920)	Novel Protein sim. GBank gil140053 sp P03764 Y401_LAMBD - HYPOTHETICAL PROTEIN ORF401	UNCLASSIFIED	1006
3145	78463749 (4367, 4368)	Novel Protein sim. GBank gil1403399 emb CAA98355 - (Z74024) hypothetical protein RV2879c [Mycobacterium tuberculosis]	UNCLASSIFIED	1026
3146	11390288 (6097, 6098)	Novel Protein sim. GBank gil140370 sp P25567 SRO9_YEAST - SRO9 - PROTEIN	UNCLASSIFIED	1024
3147	80237180 (19633, 19634)	Novel Protein sim. GBank gil140388 sp P25744 YCEE_ECOLI - HYPOTHETICAL 43.9 KD PROTEIN IN MSYB-HTRB INTERGENIC REGION (ORF1)	UNCLASSIFIED	1012, 1022
3148	78726651 (17595, 17596)	Novel Protein sim. GBank gil140395 sp P25582 YCF4_YEAST - HYPOTHETICAL 83.2 KD PROTEIN IN KAR4-PBN1 INTERGENIC REGION	UNCLASSIFIED	1003, 1022

3149	79836168 (22051, 22052)	Novel Protein sim. GBank gil140432 splP21362 YCF_ECOLI - 18.6 KD PROTEIN IN TONB-TRPA INTERGENIC REGION (ORF2)		UNCLASSIFIED	1008, 1017, 1024
3150	78768689 (5913, 5914)	Novel Protein sim. GBank gil140514 splP25355 YCU4_YEAST - HYPOTHETICAL 65.2 KD PROTEIN IN THR4- PWP2 INTERGENIC REGION		UNCLASSIFIED	1022
3151	27931399 (6385, 6386)	Novel Protein sim. GBank gil140519 splP25637 YCU9_YEAST - HYPOTHETICAL 29.0 KD PROTEIN IN PWP2- SUP61 INTERGENIC REGION		UNCLASSIFIED	1006
3152	78785575 (14365, 14366)	Novel Protein sim. GBank gil140524 splP25365 SED4_YEAST - SED4 PROTEIN		UNCLASSIFIED	1009, 1022
3153	78983343 (4361, 4362)	Novel Protein sim. GBank gil140545 splP25651 YCX6_YEAST - HYPOTHETICAL 21.7 KD PROTEIN IN TUP1- ABP1 INTERGENIC REGION		UNCLASSIFIED	1044
3154	11122448 (13203, 13204)	Novel Protein sim. GBank gil140753 splP26646 YHDH_ECOLI - HYPOTHETICAL 34.7 KD PROTEIN IN MREB- ACCB INTERGENIC REGION (ORF1)		UNCLASSIFIED	1034
3155	79113980 (16039, 16040)	Novel Protein sim. GBank gil141279 splP21260 YPRO_OWEFU - HYPOTHETICAL PROLINE-RICH PROTEIN		UNCLASSIFIED	1044
3156	9366940 (14841, 14842)	Novel Protein sim. GBank gil141307 splP24563 YPT4_PSEAE - HYPOTHETICAL 57.4 KD PROTEIN IN PILT REGION (ORF4)		UNCLASSIFIED	1017
3157	28806912 (19329, 19330)	Novel Protein sim. GBank gil141468 splP26944 YTR6_AZOBR - HYPOTHETICAL PROTEIN IN ACETYL TRANSFERASE 3'REGION (ORF6)		UNCLASSIFIED	1022

3158	79457254 (10729, 10730)	Novel Protein sim. GBank gil141617 spl P08031 ZEB2_MAIZE - ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)		UNCLASSIFIED	1024
3159	55763493 (3339, 3340)	Novel Protein sim. GBank gil1435038 dbj BAA07227 - (D38024) ORF [Homo sapiens]		UNCLASSIFIED	1023
3160	88095842 (9755, 9756)	Novel Protein sim. GBank gil145484 (M93570) - PTS enzyme III cel [Escherichia coli]		UNCLASSIFIED	1034
3161	20110065 (2533, 2534)	Novel Protein sim. GBank gil146168 (J01617) - glutaminyl-tRNA synthetase [Escherichia coli]		UNCLASSIFIED	1010
3162	32081101 (11209, 11210)	Novel Protein sim. GBank gil146168 (J01617) - glutaminyl-tRNA synthetase [Escherichia coli]		UNCLASSIFIED	1034, 1044
3163	78758201 (7131, 7132)	Novel Protein sim. GBank gil1469199 dbj BAA09487 - (D50928) The KIAA0138 gene product is novel. [Homo sapiens]		UNCLASSIFIED	1008
3164	78758215 (10153, 10154)	Novel Protein sim. GBank gil1469199 dbj BAA09487 - (D50928) The KIAA0138 gene product is novel. [Homo sapiens]		UNCLASSIFIED	1008
3165	36998849 (12181, 12182)	Novel Protein sim. GBank gil1523984 emb CAA61455.1 - (X89084) phosphate acetyltransferase [Corynebacterium glutamicum]		UNCLASSIFIED	1001
3166	78381623 (3591, 3592)	Novel Protein sim. GBank gil1524191 emb CAB02007 - (Z79700) echA7 [Mycobacterium tuberculosis]		UNCLASSIFIED	1003
3167	66694781 (6697, 6698)	Novel Protein sim. GBank gil1524205 emb CAB01993 - (Z79700) purH [Mycobacterium tuberculosis]		UNCLASSIFIED	1009
3168	79604009 (8439, 8440)	Novel Protein sim. GBank gil1524282 emb CAB02072 - (Z79702) uspC [Mycobacterium tuberculosis]		UNCLASSIFIED	1004

3169	80218307 (14651, 14652)	Novel Protein sim. GBank gij1526613[emb]CAA63821] - (X93999) alpha-2,6-sialyltransferase [Mus musculus]		UNCLASSIFIED	1004, 1006, 1010, 1017, 1022, 1024, 1034, 1039, 1044
3170	13521450 (11895, 11896)	Novel Protein sim. GBank gij1526981[emb]CAA68204] - (X99945) amino acid permease YeeF like protein [Salmonella typhimurium]		UNCLASSIFIED	1024
3171	20292840 (15159, 15160)	Novel Protein sim. GBank gij1545857 (U50396) - WbpH [Pseudomonas aeruginosa]		UNCLASSIFIED	1034
3172	94630787 (12099, 12100)	Novel Protein sim. GBank gij1545994 (U58366) - Arsh [Yersinia enterocolitica]		UNCLASSIFIED	1039
3173	20459785 (20431, 20432)	Novel Protein sim. GBank gij1549276 (U68703) - hypothetical protein YdhE [Escherichia coli]		UNCLASSIFIED	1010
3174	85548752 (7029, 7030)	Novel Protein sim. GBank gij1575515 (U64898) - thrombospondin-related anonymous protein [Plasmodium gallinaceum]		UNCLASSIFIED	1053
3175	20617093 (16857, 16858)	Novel Protein sim. GBank gij1588980[prf]2209416K - ORF 10 [Vibrio cholerae]		UNCLASSIFIED	1004
3176	65669762 (10553, 10554)	Novel Protein sim. GBank gij159159 (M76492) - beta-tubulin [Haemophilus contortus]		UNCLASSIFIED	1010
3177	94141819 (667, 668)	Novel Protein sim. GBank gij1619929 (U70932) - reverse transcriptase [Peromyscus leucopus]		UNCLASSIFIED	1044
3178	79239383 (3325, 3326)	Novel Protein sim. GBank gij1619936 (U70935) - reverse transcriptase [Peromyscus maniculatus]		UNCLASSIFIED	1038
3179	23331018 (21445, 21446)	Novel Protein sim. GBank gij1621603 (U58365) - Np20 [Pseudomonas aeruginosa]		UNCLASSIFIED	1044
3180	85809779 (3045, 3046)	Novel Protein sim. GBank gij1648881[emb]CAB03670] - (Z81331) infB [Mycobacterium tuberculosis]		UNCLASSIFIED	1048
3181	80248646 (20943, 20944)	Novel Protein sim. GBank gij1651663[dbj]BAA16591] - (D90899) iron(III) dicitrate transport system permease protein FecD, [Synechocystis sp.]		UNCLASSIFIED	1006, 1009, 1024, 1034

3182	27341911 (3271, 3272)	Novel Protein sim. GBank gjl1651671[dbj BAA16599] - (D90899) ferrichrome-iron receptor [Synechocystis sp.]	UNCLASSIFIED	1044
3183	80240187 (22173, 22174)	Novel Protein sim. GBank gjl1651866[dbj BAA16793] - (D90900) hypothetical protein [Synechocystis sp.]	UNCLASSIFIED	1010, 1024
3184	9896969 (19769, 19770)	Novel Protein sim. GBank gjl1651867[dbj BAA16794] - (D90900) hypothetical protein [Synechocystis sp.]	UNCLASSIFIED	1039
3185	11305577 (22089, 22090)	Novel Protein sim. GBank gjl1651932[dbj BAA16858] - (D90901) nitrogen fixation positive activator protein [Synechocystis sp.]	UNCLASSIFIED	1022
3186	80053608 (17799, 17800)	Novel Protein sim. GBank gjl1652128[dbj BAA17052] - (D90903) hypothetical protein [Synechocystis sp.]	UNCLASSIFIED	1004
3187	7509118 (19811, 19812)	Novel Protein sim. GBank gjl1652190[dbj BAA17114] - (D90903) Fat protein [Synechocystis sp.]	UNCLASSIFIED	1058
3188	78380222 (5887, 5888)	Novel Protein sim. GBank gjl1652433[dbj BAA17355] - (D90905) SrrA [Synechocystis sp.]	UNCLASSIFIED	1024, 1026
3189	11691417 (1039, 1040)	Novel Protein sim. GBank gjl1652490[dbj BAA17412] - (D90905) hypothetical protein [Synechocystis sp.]	UNCLASSIFIED	1034
3190	80508512 (22143, 22144)	Novel Protein sim. GBank gjl1652848[dbj BAA17766] - (D90909) DNA photolyase [Synechocystis sp.]	UNCLASSIFIED	1012
3191	79441565 (339, 340)	Novel Protein sim. GBank gjl1652973[dbj BAA17890] - (D90910) hypothetical protein [Synechocystis sp.]	UNCLASSIFIED	1024
3192	88094361 (7801, 7802)	Novel Protein sim. GBank gjl1653184[dbj BAA18100] - (D90911) hypothetical protein [Synechocystis sp.]	UNCLASSIFIED	1006, 1010, 1022, 1024, 1044
3193	54856619 (6593, 6594)	Novel Protein sim. GBank gjl1653557[dbj BAA18470] - (D90914) hypothetical protein [Synechocystis sp.]	UNCLASSIFIED	1019, 1026

3194	87458119 (18059, 18060)	Novel Protein sim. GBank gij1655665[emb]CAB03731] - (Z81368) hypothetical protein Rv2395 [Mycobacterium tuberculosis]		UNCLASSIFIED	1018, 1050
3195	80421789 (18535, 18536)	Novel Protein sim. GBank gij1655830 (U59446) - myrosinase-binding protein related protein [Brassica napus]		UNCLASSIFIED	1022, 1025, 1044
3196	13522813 (15941, 15942)	Novel Protein sim. GBank gij1666113[emb]CAB05059] - (Z82098) hypothetical protein Rv3547 [Mycobacterium tuberculosis]		UNCLASSIFIED	1024
3197	86472669 (1291, 1292)	Novel Protein sim. GBank gij1666146[emb]CAB03781] - (Z81451) hypothetical protein Rv2438c [Mycobacterium tuberculosis]		UNCLASSIFIED	1013, 1029
3198	14996187 (16231, 16232)	Novel Protein sim. GBank gij1666181[emb]CAB04762] - (Z82004) ORF9(1) [Rhodococcus erythropolis]		UNCLASSIFIED	1024
3199	19631884 (5537, 5538)	Novel Protein sim. GBank gij1666182[emb]CAB04763] - (Z82004) ORF10(1) [Rhodococcus erythropolis]		UNCLASSIFIED	1004
3200	27977959 (14813, 14814)	Novel Protein sim. GBank gij1673324[dbj]BAA10536] - (D64003) hypothetical protein [Synechocystis sp.]		UNCLASSIFIED	1006
3201	80022773 (4561, 4562)	Novel Protein sim. GBank gij1675226 (U67205) - ACF7 neural isoform 3 [Mus musculus]		UNCLASSIFIED	1034
3202	79630737 (21587, 21588)	Novel Protein sim. GBank gij1684835 (U77671) - putative ferric siderophore receptor [Bordetella bronchiseptica]		UNCLASSIFIED	1023
3203	77918414 (20051, 20052)	Novel Protein sim. GBank gij1698442 (U41417) - beta-N-acetylhexosaminidase [Vibrio furnissii]		UNCLASSIFIED	1036
3204	78911651 (10895, 10896)	Novel Protein sim. GBank gij1703082[sp]P53585[ACLY_CAEEL - PROBABLE ATP-CITRATE (PRO-S)-LYASE (CITRATE CLEAVAGE ENZYME)]		UNCLASSIFIED	1017, 1022

3205	19882359 (135, 136)	Novel Protein sim. GBank gil1703229 sp P25409 ALAT_RAT - ALANINE AMINOTRANSFERASE (GLUTAMIC-PYRUVIC TRANSAMINASE) (GPT) (GLUTAMIC-ALANINE TRANSAMINASE)		UNCLASSIFIED	1001
3206	71328014 (10829, 10830)	Novel Protein sim. GBank gil1703256 sp P54918 ALR_SYNY3 - ALANINE RACEMASE		UNCLASSIFIED	1026, 1029
3207	78676317 (2093, 2094)	Novel Protein sim. GBank gil1703287 sp Q11010 AMPN_STRLI - AMINOPEPTIDASE N (LYSYL AMINOPEPTIDASE) (LYS-AP) (ALANINE AMINOPEPTIDASE)		UNCLASSIFIED	1008
3208	36624098 (19023, 19024)	Novel Protein sim. GBank gil1703594 (U80439) - coded for by C. elegans cDNA yk7c8.5; coded for by C. elegans cDNA yk133b3.5; coded for by C. elegans cDNA yk65a4.5; coded for by C. elegans cDNA yk7c8.3; coded for by C. elegans cDNA CEESQ86F; coded for by C. elegans cDNA yk65a4.3;...		UNCLASSIFIED	1034
3209	5637974 (16507, 16508)	Novel Protein sim. GBank gil1705586 sp P52481 CAP2_RAT - ADENYLYL CYCLASE-ASSOCIATED PROTEIN 2 (CAP)		UNCLASSIFIED	1058
3210	82125417 (227, 228)	Novel Protein sim. GBank gil1705670 sp P40986 CC1_YEAST - CELL DIVISION CONTROL PROTEIN 1		UNCLASSIFIED	1001, 1003, 1004, 1006, 1010, 1016, 1017, 1022, 1024, 1044
3211	78378932 (18021, 18022)	Novel Protein sim. GBank gil1706872 sp P53603 FTCD_PIG - FORMIMINOTRANSFERASE- CYCLODEAMINASE (FTCD) (GLUTAMATE FORMIMINOTRANSFERASE (GLUTAMATE FORMYL TRANSFERASE) / FORMIMINOTETRAHYDROFOLATE CYCLODEAMINASE		UNCLASSIFIED	1003

3212	95009485 (10877, 10878)	Novel Protein sim. GBank gil1707646[emb CAA67865] - (X99514) oprN [Pseudomonas aeruginosa]		UNCLASSIFIED	1039
3213	79626814 (16673, 16674)	Novel Protein sim. GBank gil1708007[sp P50457 GOAG_ECOLI - 4-AMINOBUTYRATE AMINOTRANSFERASE (GAMMA-AMINO-N-BUTYRATE TRANSAMINASE) (GABA TRANSAMINASE) (GLUTAMATE-SUCCINIC SEMIALDEHYDE TRANSAMINASE) (GABA AMINOTRANSFERASE)		UNCLASSIFIED	1004
3214	65848327 (4933, 4934)	Novel Protein sim. GBank gil1708021[sp P51653 GPC2_RAT - GLYPICAN-2 PRECURSOR (CEREBROGLYCAN) (HSPG M13)		UNCLASSIFIED	1025, 1054
3215	20378295 (5639, 5640)	Novel Protein sim. GBank gil1708180[sp Q10602 HEMK_MYCTU - HEMK PROTEIN HOMOLOG		UNCLASSIFIED	1004
3216	79470088 (3985, 3986)	Novel Protein sim. GBank gil1708195[sp P51979 HFM1_YEAST - HFM1 PROTEIN		UNCLASSIFIED	1022
3217	79565151 (20551, 20552)	Novel Protein sim. GBank gil1709029[sp P53258 MIC1_YEAST - MIC1 PROTEIN		UNCLASSIFIED	1023
3218	7432119 (7989, 7990)	Novel Protein sim. GBank gil1709062[sp P50108 MN10_YEAST - GALACTOSYL TRANSFERASE MN10 (BUD EMERGENCE DELAY PROTEIN 1)		UNCLASSIFIED	1058
3219	78498031 (18573, 18574)	Novel Protein sim. GBank gil1709250[sp P46935 NED4_MOUSE - NEDD-4 PROTEIN		UNCLASSIFIED	1008, 1026
3220	87123187 (5819, 5820)	Novel Protein sim. GBank gil1710106[sp Q10606 RFE_MYCTU - PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE		UNCLASSIFIED	1007, 1012, 1022, 1023, 1026, 1029, 1030, 1034

3221	80229862 (1267, 1268)	Novel Protein sim. GBank gij1710241 (U79274) - unknown [Homo sapiens]		UNCLASSIFIED	1022, 1024, 1034, 1038
3222	11286147 (22271, 22272)	Novel Protein sim. GBank gij171057 (M29146) - alpha-mannosidase [Saccharomyces cerevisiae]		UNCLASSIFIED	1006, 1058
3223	848632 (3269, 3270)	Novel Protein sim. GBank gij1710594 sp P53552 RLR1_YEAST - RLR1 PROTEIN		UNCLASSIFIED	1022
3224	82335498 (11549, 11550)	Novel Protein sim. GBank gij1710803 sp P32608 RTG2_YEAST - RETROGRADE REGULATION PROTEIN 2		UNCLASSIFIED	1001, 1003, 1004, 1006, 1008, 1009, 1010, 1016, 1017, 1022, 1024, 1029, 1034, 1044
3225	21629450 (3033, 3034)	Novel Protein sim. GBank gij1711345 sp P53012 SCS3_YEAST - SCS3 PROTEIN		UNCLASSIFIED	1008, 1034
3226	11611950 (771, 772)	Novel Protein sim. GBank gij1711360 sp P55021 SECA_STRLI - PREPROTEIN TRANSLOCASE SECA SUBUNIT		UNCLASSIFIED	1006
3227	13517742 (6451, 6452)	Novel Protein sim. GBank gij1711360 sp P55021 SECA_STRLI - PREPROTEIN TRANSLOCASE SECA SUBUNIT		UNCLASSIFIED	1024
3228	52563118 (21539, 21540)	Novel Protein sim. GBank gij1711564 sp P15589 STS_RAT - STERYL-SULFATASE PRECURSOR (STEROID SULFATASE) (STERYL-SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC)		UNCLASSIFIED	1006, 1026
3229	30005352 (8115, 8116)	Novel Protein sim. GBank gij171485 (L07289) - ESP1 gene product [Saccharomyces cerevisiae]		UNCLASSIFIED	1009

3230	79448778 (15853, 15864)	Novel Protein sim. GBank gij171615 (J03609) - nucleotide-binding regulatory protein GPA2 [Saccharomyces cerevisiae]		UNCLASSIFIED	1008, 1034
3231	56145263 (2451, 2452)	Novel Protein sim. GBank gij1718245 (U69488) - viral envelope like protein [Mus musculus]		UNCLASSIFIED	1008
3232	80054070 (235, 236)	Novel Protein sim. GBank gij171940 (M84455) - leucine zipper protein [Saccharomyces cerevisiae]		UNCLASSIFIED	1017, 1022
3233	82112527 (7383, 7384)	Novel Protein sim. GBank gij171940 (M84455) - leucine zipper protein [Saccharomyces cerevisiae]		UNCLASSIFIED	1003, 1006, 1008, 1016, 1017, 1022, 1024, 1027, 1034, 1038, 1039
3234	80052380 (2887, 2888)	Novel Protein sim. GBank gij172094 (M36822) - SIN3 open reading frame [Saccharomyces cerevisiae]		UNCLASSIFIED	1003, 1004, 1010
3235	80500184 (6607, 6608)	Novel Protein sim. GBank gij1722927 [sp Q10403 Y00R_MYCTU - HYPOTHETICAL 31.7 KD PROTEIN CY190.27		UNCLASSIFIED	1003, 1004, 1006, 1010, 1012, 1017, 1024, 1030, 1034, 1039
3236	78676067 (6017, 6018)	Novel Protein sim. GBank gij1722945 [sp Q10523 Y01N_MYCTU - HYPOTHETICAL 44.6 KD PROTEIN CY427.23		UNCLASSIFIED	1008
3237	82124947 (17637, 17638)	Novel Protein sim. GBank gij1722977 [sp Q10638 Y03C_MYCTU - HYPOTHETICAL 82.8 KD PROTEIN CY130.12C		UNCLASSIFIED	1004, 1006, 1008, 1010, 1016, 1022, 1029
3238	79914416 (18307, 18308)	Novel Protein sim. GBank gij1723026 [sp Q10897 Y05L_MYCTU - HYPOTHETICAL 70.4 KD PROTEIN CY251.21		UNCLASSIFIED	1001
3239	47652140 (11739, 11740)	Novel Protein sim. GBank gij1723065 [sp Q11030 Y07O_MYCTU - HYPOTHETICAL 37.3 KD PROTEIN CY02B10.24 PRECURSOR		UNCLASSIFIED	1029

3240	79589353 (19353, 19354)	Novel Protein sim. GBank gij1723092 sp Q11059 Y08N_MYCTU - HYPOTHETICAL 37.0 KD PROTEIN CY50.23C		UNCLASSIFIED	1010, 1038
3241	80218509 (19505, 19506)	Novel Protein sim. GBank gij1723189 sp P39731 YADA_YEAST - HYPOTHETICAL 33.2 KD PROTEIN IN PYK1- SNC1 INTERGENIC REGION		UNCLASSIFIED	1010, 1017, 1022, 1024, 1025, 1031, 1034, 1044
3242	80250304 (1989, 1990)	Novel Protein sim. GBank gij1723558 sp Q10449 YDEG_SCHPO - HYPOTHETICAL 57.2 KD PROTEIN C12B10.16C IN CHROMOSOME I		UNCLASSIFIED	1006
3243	80229661 (19319, 19320)	Novel Protein sim. GBank gij1723543 sp P53204 YG15_YEAST - HYPOTHETICAL 44.9 KD PROTEIN IN SEC9- MSB2 INTERGENIC REGION		UNCLASSIFIED	1003, 1024, 1044
3244	27842185 (15643, 15644)	Novel Protein sim. GBank gij1723650 sp P53212 YG1D_YEAST - HYPOTHETICAL 31.7 KD PROTEIN IN VMA7- RPS31A INTERGENIC REGION		UNCLASSIFIED	1004, 1006, 1010, 1022, 1034
3245	79608932 (13893, 13894)	Novel Protein sim. GBank gij1723688 sp P53255 YG2M_YEAST - HYPOTHETICAL 58.2 KD PROTEIN IN DBF2- VAS1 INTERGENIC REGION		UNCLASSIFIED	1034
3246	80478615 (7461, 7462)	Novel Protein sim. GBank gij1723699 sp P53267 YG2Y_YEAST - HYPOTHETICAL 37.8 KD PROTEIN IN CLB6- SPT6 INTERGENIC REGION		UNCLASSIFIED	1001, 1003, 1004, 1006, 1008, 1010, 1012, 1017, 1022, 1024, 1025, 1027, 1034
3247	80219848 (18267, 18268)	Novel Protein sim. GBank gij1723699 sp P53267 YG2Y_YEAST - HYPOTHETICAL 37.8 KD PROTEIN IN CLB6- SPT6 INTERGENIC REGION		UNCLASSIFIED	1001, 1003, 1004, 1006, 1010, 1022, 1024, 1034, 1039

3248	9899921 (10627, 10628)	Novel Protein sim. GBank gil1723811 sp P55135 YGCA_ECOLI - HYPOTHETICAL RNA METHYLTRANSFERASE IN RELA-BARA INTERGENIC REGION		UNCLASSIFIED	1039
3249	80016773 (18085, 18086)	Novel Protein sim. GBank gil1723900 sp P53140 YGK7_YEAST - HYPOTHETICAL 74.6 KD PROTEIN IN TAF60- G4P1 INTERGENIC REGION		UNCLASSIFIED	1001, 1006, 1010, 1012, 1022
3250	29235305 (6345, 6346)	Novel Protein sim. GBank gil1723969 sp P53075 YGX8_YEAST - HYPOTHETICAL 66.9 KD PROTEIN IN SAP4- OST5 INTERGENIC REGION		UNCLASSIFIED	1008
3251	95011210 (21421, 21422)	Novel Protein sim. GBank gil1723977 sp P53067 YGZ1_YEAST - HYPOTHETICAL 113.9 KD PROTEIN IN RTF1- CSE1 INTERGENIC REGION		UNCLASSIFIED	1001, 1008, 1022, 1038
3252	11612706 (6357, 6358)	Novel Protein sim. GBank gil1723981 sp P53063 YGZ6_YEAST - HYPOTHETICAL 44.5 KD PROTEIN IN PDE1- RTF1 INTERGENIC REGION		UNCLASSIFIED	1006
3253	24122000 (1697, 1698)	Novel Protein sim. GBank gil1729784 emb CAA70932 - (Y09798) colS [Pseudomonas fluorescens]		UNCLASSIFIED	1044
3254	78300843 (8207, 8208)	Novel Protein sim. GBank gil1730203 sp P50442 GATM_RAT - GLYCINE AMIDINOTRANSFERASE PRECURSOR (L- ARGININE:GLYCINE AMIDINOTRANSFERASE) (TRANSAMIDINASE) (AT)		UNCLASSIFIED	1026, 1030
3255	57303999 (16043, 16044)	Novel Protein sim. GBank gil1730592 sp P49954 YL85_YEAST - HYPOTHETICAL 32.5 KD PROTEIN YLR351C		UNCLASSIFIED	1034
3256	79776164 (1177, 1178)	Novel Protein sim. GBank gil1730621 sp P53759 YMI0_YEAST - HYPOTHETICAL 48.1 KD PROTEIN IN TUB1- CPR3 INTERGENIC REGION		UNCLASSIFIED	1003, 1008

3257	20705686 (7727, 7728)	Novel Protein sim. GBank gil1730632 sp P50104 YMP9_YEAST - PUTATIVE 109.8 KD TRANSCRIPTIONAL REGULATORY PROTEIN IN SOK2-FMS1 INTERGENIC REGION		UNCLASSIFIED	1034
3258	78444803 (12925, 12926)	Novel Protein sim. GBank gil1730647 sp P53832 YN23_YEAST - HYPOTHETICAL 52.3 KD PROTEIN IN MRPL10- ERG24 INTERGENIC REGION PRECURSOR		UNCLASSIFIED	1026
3259	71088488 (18455, 18456)	Novel Protein sim. GBank gil1730647 sp P53832 YN23_YEAST - HYPOTHETICAL 52.3 KD PROTEIN IN MRPL10- ERG24 INTERGENIC REGION PRECURSOR		UNCLASSIFIED	1029, 1053
3260	80218785 (10043, 10044)	Novel Protein sim. GBank gil1730655 sp P53824 SNZ2_YEAST - SNZ2 PROTEIN		UNCLASSIFIED	1003, 1006, 1010, 1022, 1024, 1031, 1034
3261	80219860 (21489, 21490)	Novel Protein sim. GBank gil1730730 sp P53954 ALGB_YEAST - ALG11 PROTEIN		UNCLASSIFIED	1004, 1006, 1009, 1010, 1024
3262	78725687 (20185, 20186)	Novel Protein sim. GBank gil1730733 sp P53951 YNF1_YEAST - HYPOTHETICAL 45.6 KD PROTEIN IN COX5A- ALG11 INTERGENIC REGION		UNCLASSIFIED	1022
3263	79600647 (18433, 18434)	Novel Protein sim. GBank gil1730746 sp P53939 YNH8_YEAST - HYPOTHETICAL 45.9 KD PROTEIN IN TPM1- MKS1 INTERGENIC REGION		UNCLASSIFIED	1006
3264	80219252 (1085, 1086)	Novel Protein sim. GBank gil1730751 sp P53935 YNJ1_YEAST - HYPOTHETICAL 141.5 KD PROTEIN IN YPT53- RHO2 INTERGENIC REGION		UNCLASSIFIED	1001, 1003, 1004, 1006, 1008, 1009, 1010, 1016, 1017, 1022, 1023, 1024, 1031, 1034, 1039, 1044

3265	38909150 (19221, 19222)	Novel Protein sim. GBank gil1730764 sp P53927 YNL0_YEAST - HYPOTHETICAL 25.4 KD PROTEIN IN CYB5- LEU4 INTERGENIC REGION		UNCLASSIFIED	1008
3266	80236379 (3495, 3496)	Novel Protein sim. GBank gil1730773 sp P53918 YNNM5_YEAST - HYPOTHETICAL 73.8 KD PROTEIN IN SPC98- TOM70 INTERGENIC REGION		UNCLASSIFIED	1008, 1009, 1022, 1024
3267	27959515 (21835, 21836)	Novel Protein sim. GBank gil1730779 sp P53912 YNN4_YEAST - HYPOTHETICAL 41.2 KD PROTEIN IN FPR1- TOM22 INTERGENIC REGION		UNCLASSIFIED	1006
3268	25324266 (7897, 7898)	Novel Protein sim. GBank gil1730799 sp P53890 YNQ6_YEAST - HYPOTHETICAL 49.7 KD PROTEIN IN SKO1- RPL44A INTERGENIC REGION		UNCLASSIFIED	1017
3269	20182193 (17951, 17952)	Novel Protein sim. GBank gil1730815 sp P53873 YNS7_YEAST - HYPOTHETICAL 40.3 KD PROTEIN IN KAR1- UBP10 INTERGENIC REGION		UNCLASSIFIED	1024
3270	79556251 (19679, 19680)	Novel Protein sim. GBank gil1730823 sp P53868 ALG9_YEAST - PROBABLE MANNOSYLTRANSFERASE ALG9		UNCLASSIFIED	1025
3271	56011990 (11911, 11912)	Novel Protein sim. GBank gil1731071 sp P54545 YQJH_BACSU - HYPOTHETICAL 47.0 KD PROTEIN IN GLNQ- ANSR INTERGENIC REGION		UNCLASSIFIED	1008
3272	78082991 (975, 976)	Novel Protein sim. GBank gil1731094 sp P54571 YQKI_BACSU - HYPOTHETICAL NA+/H+ ANTIporter IN ANSB-SPOIIM INTERGENIC REGION		UNCLASSIFIED	1029
3273	20731645 (6543, 6544)	Novel Protein sim. GBank gil1731125 sp P54433 YRKE_BACSU - HYPOTHETICAL 20.7 KD PROTEIN IN BLTR- SPOIIC INTERGENIC REGION		UNCLASSIFIED	1034

3274	80258978 (16471, 16472)	Novel Protein sim. GBank gi 1731287 sp Q10818 YX28_MYCTU - HYPOTHETICAL 52.9 KD PROTEIN CY274.28C		UNCLASSIFIED	1022, 1026, 1030
3275	20724406 (11513, 11514)	Novel Protein sim. GBank gi 1731295 sp Q10827 YX42_MYCTU - HYPOTHETICAL 17.0 KD PROTEIN CY274.42C		UNCLASSIFIED	1006
3276	54656911 (17059, 17060)	Novel Protein sim. GBank gi 1731438 sp P51504 ZN80_HUMAN - ZINC FINGER PROTEIN 80 (ZNFPT17)		UNCLASSIFIED	1022
3277	5628381 (13397, 13398)	Novel Protein sim. GBank gi 173164 (J02719) - valyl-tRNA synthetase [Saccharomyces cerevisiae]		UNCLASSIFIED	1058
3278	79625428 (507, 508)	Novel Protein sim. GBank gi 173177 (L02869) - VPS17 [Saccharomyces cerevisiae]		UNCLASSIFIED	1006, 1022, 1023, 1026, 1044
3279	80232516 (18025, 18026)	Novel Protein sim. GBank gi 1736514 db BAA15678 - (D90829) [isochorismatase (EC 3.2.2.1) (2,3 dihydro-2,3 dihydroxybenzoate synthase). [Escherichia coli]]		UNCLASSIFIED	1022
3280	82021119 (10167, 10168)	Novel Protein sim. GBank gi 1742619 db BAA15320 - (D90801) Bicyclomycin resistance protein (Sulfonamide resistance protein). [Escherichia coli]		UNCLASSIFIED	1003, 1006, 1010, 1016, 1022, 1023, 1026, 1029, 1039, 1049, 1054
3281	52560843 (16125, 16126)	Novel Protein sim. GBank gi 1742728 db BAA15421 - (D90809) Chitinase 3 precursor (EC 3.2.1.14). [Escherichia coli]		UNCLASSIFIED	1017
3282	80428437 (7339, 7340)	Novel Protein sim. GBank gi 1742766 db BAA15457 - (D90811) Nifs protein. [Escherichia coli]		UNCLASSIFIED	1023, 1025, 1054
3283	27980533 (14451, 14452)	Novel Protein sim. GBank gi 1750108 (U66480) - YnbA [Bacillus subtilis]		UNCLASSIFIED	1006
3284	79551776 (21291, 21292)	Novel Protein sim. GBank gi 1753160 (U79564) - unidentified ferric siderophore receptor [Bordetella bronchiseptica]		UNCLASSIFIED	1001

3285	55310325 (12997, 12998)	Novel Protein sim. GBank gij1754627[dbj BAA13116] - (D86566) NOTCH4 [Homo sapiens]		UNCLASSIFIED	1019
3286	17650051 (21473, 21474)	Novel Protein sim. GBank gij1763011 (U67963) - lysophospholipase homolog [Homo sapiens]		UNCLASSIFIED	1017
3287	79179312 (2357, 2358)	Novel Protein sim. GBank gij1780764[emb CAA71456] - (Y10435) translated orf similarity to SWISS-PROT: SYGA_ECOLI glycyl-tRNA synthetase alpha-chain [Coxiella burnetii]		UNCLASSIFIED	1024
3288	20742752 (18699, 18700)	Novel Protein sim. GBank gij1781050[emb CAB06186] - (Z83863) aroE [Mycobacterium tuberculosis]		UNCLASSIFIED	1022
3289	79764293 (7335, 7336)	Novel Protein sim. GBank gij1781122[emb CAB06206] - (Z83864) hypothetical protein Rv3835 [Mycobacterium tuberculosis]		UNCLASSIFIED	1023, 1034, 1044
3290	95293316 (16855, 16856)	Novel Protein sim. GBank gij1781144[emb CAB06254] - (Z83866) hypothetical protein Rv3069 [Mycobacterium tuberculosis]		UNCLASSIFIED	1024
3291	20402955 (22433, 22434)	Novel Protein sim. GBank gij1781185[emb CAB06125] - (Z83859) adhA [Mycobacterium tuberculosis]		UNCLASSIFIED	1004
3292	65707949 (5475, 5476)	Novel Protein sim. GBank gij1787094 (AE000188) - putative dTDP-glucose enzyme [Escherichia coli]		UNCLASSIFIED	1023, 1031
3293	91228207 (6809, 6810)	Novel Protein sim. GBank gij1787243 (AE000202) - putative enzyme [Escherichia coli]		UNCLASSIFIED	1003
3294	13022355 (10073, 10074)	Novel Protein sim. GBank gij1787247 (AE000202) - orf, hypothetical protein [Escherichia coli]		UNCLASSIFIED	1024
3295	79863168 (3073, 3074)	Novel Protein sim. GBank gij1787723 (AE000242) - putative outer membrane receptor for iron transport [Escherichia coli]		UNCLASSIFIED	1017

3296	17710632 (6727, 6728)	Novel Protein sim. GBank gij1787723 (AE000242) - putative outer membrane receptor for iron transport [Escherichia coli]		UNCLASSIFIED	1044
3297	10050612 (7459, 7460)	Novel Protein sim. GBank gij1787724 (AE000242) - putative receptor [Escherichia coli]		UNCLASSIFIED	1017
3298	8355488 (21367, 21368)	Novel Protein sim. GBank gij1788590 (AE000315) - orf, hypothetical protein [Escherichia coli]		UNCLASSIFIED	1008, 1022
3299	78677629 (17171, 17172)	Novel Protein sim. GBank gij1788627 (AE000318) - putative aminotransferase [Escherichia coli]		UNCLASSIFIED	1009
3300	20396139 (3733, 3734)	Novel Protein sim. GBank gij1788770 (AE000330) - putative beta-lactamase [Escherichia coli]		UNCLASSIFIED	1004
3301	79639423 (17999, 18000)	Novel Protein sim. GBank gij1789035 (AE000352) - orf, hypothetical protein [Escherichia coli]		UNCLASSIFIED	1003
3302	13515530 (14619, 14620)	Novel Protein sim. GBank gij1789036 (AE000352) - putative transport protein [Escherichia coli]		UNCLASSIFIED	1024
3303	20445442 (15505, 15506)	Novel Protein sim. GBank gij1790277 (AE000459) - putative oxidoreductase [Escherichia coli]		UNCLASSIFIED	1010
3304	70945165 (21919, 21920)	Novel Protein sim. GBank gij1794165 [BAA11215] - (D78137) Na+/glucose symporter [Vibrio parahaemolyticus]		UNCLASSIFIED	1029
3305	77539953 (6019, 6020)	Novel Protein sim. GBank gij1800301 (U83667) - macrolide-efflux determinant [Streptococcus pneumoniae]		UNCLASSIFIED	1016
3306	20451216 (15991, 15992)	Novel Protein sim. GBank gij1817699 [emb] CAB06573] - (Z84724) hypothetical protein Rv0433 [Mycobacterium tuberculosis]		UNCLASSIFIED	1024

3307	25252782 (5691, 5692)	Novel Protein sim. GBank gil1817714[emb]CAB06590] - (Z84725) lpqK [Mycobacterium tuberculosis]		UNCLASSIFIED	1008
3308	32302946 (10315, 10316)	Novel Protein sim. GBank gil1834376[emb]CAA70860] - (Y09666) RagB [Bradyrhizobium japonicum]		UNCLASSIFIED	1029
3309	80504793 (22535, 22536)	Novel Protein sim. GBank gil1838990[emb]CAB06634] - (Z85982) hypothetical protein Rv1839c [Mycobacterium tuberculosis]		UNCLASSIFIED	1012
3310	20465379 (9341, 9342)	Novel Protein sim. GBank gil1838991[emb]CAB06635] - (Z85982) lysX [Mycobacterium tuberculosis]		UNCLASSIFIED	1010
3311	66490267 (15309, 15310)	Novel Protein sim. GBank gil1842429 (U81036) - ankyrin binding cell adhesion molecule neurofascin [Rattus norvegicus]		UNCLASSIFIED	1010, 1029
3312	79561132 (1237, 1238)	Novel Protein sim. GBank gil1848058[dbj]BAA11346] - (D78321) pyrimidine dimer DNA glycosylase [Micrococcus luteus]		UNCLASSIFIED	1038
3313	37034313 (19689, 19690)	Novel Protein sim. GBank gil1850114[emb]CAB06681] - (Z86089) hypothetical protein Rv0269c [Mycobacterium tuberculosis]		UNCLASSIFIED	1012
3314	86688766 (12397, 12398)	Novel Protein sim. GBank gil186396 (M94131) - mucin [Homo sapiens]		UNCLASSIFIED	1018, 1024, 1029, 1038
3315	54534348 (7103, 7104)	Novel Protein sim. GBank gil186398 (M94132) - MUC2 [Homo sapiens]		UNCLASSIFIED	1041
3316	27977681 (321, 322)	Novel Protein sim. GBank gil1870004[emb]CAB06855] - (Z92539) hypothetical protein Rv1024 [Mycobacterium tuberculosis]		UNCLASSIFIED	1006
3317	19536322 (5025, 5026)	Novel Protein sim. GBank gil1870004[emb]CAB06855] - (Z92539) hypothetical protein Rv1024 [Mycobacterium tuberculosis]		UNCLASSIFIED	1039

3318	79862802 (13485, 13486)	Novel Protein sim. GBank gi 1877268 emb CAB07049 - (Z92770) hypothetical protein Rv0143c [Mycobacterium tuberculosis]		UNCLASSIFIED	1010, 1012, 1049
3319	14988129 (10937, 10938)	Novel Protein sim. GBank gi 1877371 emb CAB07123 - (Z92772) hypothetical protein Rv0634c [Mycobacterium tuberculosis]		UNCLASSIFIED	1001
3320	80075653 (12217, 12218)	Novel Protein sim. GBank gi 188864 (M74027) - mucin [Homo sapiens]		UNCLASSIFIED	1017, 1034
3321	9674619 (22667, 22668)	Novel Protein sim. GBank gi 1905993 (U89712) - putative 3-(3-hydroxyphenyl) propionate transport protein; HppK [Rhodococcus globerulus]		UNCLASSIFIED	1034
3322	20586591 (1551, 1552)	Novel Protein sim. GBank gi 1934732 (U96128) - UDP-galactopyranose mutase [Mycobacterium tuberculosis]		UNCLASSIFIED	1022
3323	20544489 (11809, 11810)	Novel Protein sim. GBank gi 1947160 (AF000298) - weak similarity to collagens; glycine- and proline-rich [Caenorhabditis elegans]		UNCLASSIFIED	1058
3324	78726670 (19809, 19810)	Novel Protein sim. GBank gi 1947160 (AF000298) - weak similarity to collagens; glycine- and proline-rich [Caenorhabditis elegans]		UNCLASSIFIED	1008, 1054
3325	90999628 (7327, 7328)	Novel Protein sim. GBank gi 198646 (M29324) - ORF2; 5' end undetermined. [Mus musculus]		UNCLASSIFIED	1020
3326	20467349 (763, 764)	Novel Protein sim. GBank gi 2039375 (U97405) - T09B4.5 gene product [Caenorhabditis elegans]		UNCLASSIFIED	1010
3327	65484068 (10063, 10064)	Novel Protein sim. GBank gi 2047346 (AF000198) - Similar to cuticular collagen [Caenorhabditis elegans]		UNCLASSIFIED	1001, 1023
3328	80236408 (16339, 16340)	Novel Protein sim. GBank gi 2055394 (U87306) - transmembrane receptor UNC5H2 [Rattus norvegicus]		UNCLASSIFIED	1004, 1006, 1010, 1022, 1023, 1024, 1034

3329	55860027 (16111, 16112)	Novel Protein sim. GBank gil2065209[emb]CAA73250] - (Y12713) Gag polyprotein [Mus musculus]		UNCLASSIFIED	1038
3330	78391858 (16961, 16962)	Novel Protein sim. GBank gil2065210[emb]CAA73251] - (Y12713) Pro-Pol- dUTPase polyprotein [Mus musculus]		UNCLASSIFIED	1030
3331	79474456 (17017, 17018)	Novel Protein sim. GBank gil2065210[emb]CAA73251] - (Y12713) Pro-Pol- dUTPase polyprotein [Mus musculus]		UNCLASSIFIED	1038
3332	20746461 (21773, 21774)	Novel Protein sim. GBank gil2065210[emb]CAA73251] - (Y12713) Pro-Pol- dUTPase polyprotein [Mus musculus]		UNCLASSIFIED	1004
3333	86666767 (21889, 21890)	Novel Protein sim. GBank gil2072719[emb]CAB08323] - (Z95121) hypothetical protein Rv3252c [Mycobacterium tuberculosis]		UNCLASSIFIED	1029
3334	86684161 (9373, 9374)	Novel Protein sim. GBank gil2072966 (U93570) - p40 [Homo sapiens]		UNCLASSIFIED	1029
3335	65881389 (21373, 21374)	Novel Protein sim. GBank gil2072967 (U93570) - putative p150 [Homo sapiens]		UNCLASSIFIED	1054
3336	78376411 (2139, 2140)	Novel Protein sim. GBank gil2076703[emb]CAB08362] - (Z95150) hypothetical protein Rv3129 [Mycobacterium tuberculosis]		UNCLASSIFIED	1008, 1026
3337	88097287 (6161, 6162)	Novel Protein sim. GBank gil2078009[emb]CAB08456] - (Z95207) hypothetical protein Rv2850c [Mycobacterium tuberculosis]		UNCLASSIFIED	1008, 1013, 1018, 1019, 1025, 1026, 1029, 1053, 1054
3338	80052457 (1105, 1106)	Novel Protein sim. GBank gil2078027[emb]CAB08467] - (Z95208) hypothetical protein Rv2372c [Mycobacterium tuberculosis]		UNCLASSIFIED	1010, 1017
3339	82103445 (16203, 16204)	Novel Protein sim. GBank gil2078037[emb]CAB08461] - (Z95208) hypothetical protein Rv2362c [Mycobacterium tuberculosis]		UNCLASSIFIED	1003, 1004, 1016, 1017, 1022, 1024

3340	77887412 (8899, 8900)	Novel Protein sim. GBank gil2078043[emb]CAB08466] - (Z95208) glyS [Mycobacterium tuberculosis]		UNCLASSIFIED	1023
3341	79167914 (19061, 19062)	Novel Protein sim. GBank gil2088651 (AF002109) - hypersensitivity-related gene 201 Isolog [Arabidopsis thaliana]		UNCLASSIFIED	1031, 1050
3342	80504299 (14935, 14936)	Novel Protein sim. GBank gil208931 (M15619) - ORF16-lacZ fusion protein [Artificial gene]		UNCLASSIFIED	1012
3343	17679564 (20209, 20210)	Novel Protein sim. GBank gil2104302[emb]CAB08631] - (Z95387) hypothetical protein Rv2611c [Mycobacterium tuberculosis]		UNCLASSIFIED	1008
3344	78386187 (21501, 21502)	Novel Protein sim. GBank gil2104315[emb]CAB08664] - (Z95388) pbpB [Mycobacterium tuberculosis]		UNCLASSIFIED	1008
3345	79911261 (20103, 20104)	Novel Protein sim. GBank gil2104343[emb]CAB08658] - (Z95388) hypothetical protein Rv2135c [Mycobacterium tuberculosis]		UNCLASSIFIED	1012
3346	88094709 (15027, 15028)	Novel Protein sim. GBank gil2104362[emb]CAB08690] - (Z95389) mrsA [Mycobacterium tuberculosis]		UNCLASSIFIED	1004
3347	79872123 (18527, 18528)	Novel Protein sim. GBank gil2104388[emb]CAB08729] - (Z95390) hypothetical protein Rv3463 [Mycobacterium tuberculosis]		UNCLASSIFIED	1044
3348	78993157 (905, 906)	Novel Protein sim. GBank gil2104465[emb]CAB08775] - (Z95397) unknown [Schizosaccharomyces pombe]		UNCLASSIFIED	1039
3349	20294822 (21981, 21992)	Novel Protein sim. GBank gil2105045[emb]CAB08839] - (Z95436) hypothetical protein Rv3649 [Mycobacterium tuberculosis]		UNCLASSIFIED	1034
3350	79413002 (14019, 14020)	Novel Protein sim. GBank gil2113919[emb]CAB08888] - (Z95554) hypothetical protein Rv1635c [Mycobacterium tuberculosis]		UNCLASSIFIED	1024

3351	78475152 (16965, 16966)	Novel Protein sim. GBank gil2113941[emb CAB08926] - (Z95556) hypothetical protein RV2508c [Mycobacterium tuberculosis]		UNCLASSIFIED	1003, 1006
3352	78368412 (5391, 5392)	Novel Protein sim. GBank gil2114020[emb CAB08969] - (Z95558) ubIE [Mycobacterium tuberculosis]		UNCLASSIFIED	1003
3353	19520527 (1333, 1334)	Novel Protein sim. GBank gil2114024[emb CAB08957] - (Z95558) grcC1 [Mycobacterium tuberculosis]		UNCLASSIFIED	1022
3354	78459337 (8593, 8594)	Novel Protein sim. GBank gil2114321[dbj BAA20037] - (D88733) membrane glycoprotein [Equine herpesvirus 1]		UNCLASSIFIED	1016, 1026, 1029
3355	80258073 (11169, 11170)	Novel Protein sim. GBank gil2114321[dbj BAA20037] - (D88733) membrane glycoprotein [Equine herpesvirus 1]		UNCLASSIFIED	1010
3356	11669239 (16597, 16598)	Novel Protein sim. GBank gil2114321[dbj BAA20037] - (D88733) membrane glycoprotein [Equine herpesvirus 1]		UNCLASSIFIED	1024
3357	99277458 (16935, 16936)	Novel Protein sim. GBank gil2114323[dbj BAA20038] - (D88734) membrane glycoprotein [Equine herpesvirus 1]		UNCLASSIFIED	1001, 1003, 1004, 1008, 1009, 1010, 1017, 1022, 1023, 1031, 1034, 1037, 1038, 1039, 1040, 1044, 1049, 1053, 1054
3358	56718862 (10925, 10926)	Novel Protein sim. GBank gil2114473 (U96963) - p140mDia [Mus musculus]		UNCLASSIFIED	1000, 1017
3359	12882700 (18713, 18714)	Novel Protein sim. GBank gil2117191[emb CAB09012] - (Z95584) omt [Mycobacterium tuberculosis]		UNCLASSIFIED	1031
3360	27954841 (657, 658)	Novel Protein sim. GBank gil2117310[emb CAB09116.1] - (Z95620) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	1022

3361	80080798 (1645, 1646)	Novel Protein sim. GBank gij2117310[emb]CAB09116.1] - (Z95620) hypothetical protein [Schizosaccharomyces pombe]	UNCLASSIFIED	1023, 1034
3362	20297171 (3101, 3102)	Novel Protein sim. GBank gij2117310[emb]CAB09116.1] - (Z95620) hypothetical protein [Schizosaccharomyces pombe]	UNCLASSIFIED	1034
3363	80049510 (20545, 20546)	Novel Protein sim. GBank gij2117310[emb]CAB09116.1] - (Z95620) hypothetical protein [Schizosaccharomyces pombe]	UNCLASSIFIED	1010
3364	79444139 (9831, 9832)	Novel Protein sim. GBank gij2120075[pir]S89966 - TyB protein - yeast (Saccharomyces cerevisiae) retrotransposon Ty2.L	UNCLASSIFIED	1003, 1008, 1010
3365	34623202 (4159, 4160)	Novel Protein sim. GBank gij2120083[pir]I38588 - transposon LRE2 reverse transcriptase homolog - human	UNCLASSIFIED	1029
3366	78380212 (4809, 4810)	Novel Protein sim. GBank gij2127337[pir]I40661 - methylaspartate mutase (EC 5.4.99.1) component L - Clostridium cochlearium	UNCLASSIFIED	1026
3367	78795030 (12323, 12324)	Novel Protein sim. GBank gij2127352[pir]I40866 - exo-alpha-sialidase (EC 3.2.1.18) - Clostridium perfringens	UNCLASSIFIED	1008, 1022, 1053
3368	80502586 (15215, 15216)	Novel Protein sim. GBank gij2127352[pir]I40866 - exo-alpha-sialidase (EC 3.2.1.18) - Clostridium perfringens	UNCLASSIFIED	1012, 1023, 1024, 1036
3369	79610404 (8339, 8340)	Novel Protein sim. GBank gij2127414[pir]S60064 - hypothetical protein 2 - Corynebacterium glutamicum	UNCLASSIFIED	1004
3370	39290717 (22223, 22224)	Novel Protein sim. GBank gij2128914[pir]F64489 - hypothetical protein MJ1519 - Methanococcus jannaschii	UNCLASSIFIED	1029

3371	30656520 (10363, 10364)	Novel Protein sim. GBank gjl2129003 pir G64507 - hypothetical protein MJ1665 - Methanococcus jannaschii	UNCLASSIFIED	1026
3372	79399335 (16829, 16830)	Novel Protein sim. GBank gjl2129003 pir G64507 - hypothetical protein MJ1665 - Methanococcus jannaschii	UNCLASSIFIED	1024
3373	79582628 (16871, 16872)	Novel Protein sim. GBank gjl2129003 pir G64507 - hypothetical protein MJ1665 - Methanococcus jannaschii	UNCLASSIFIED	1027
3374	47656049 (3687, 3688)	Novel Protein sim. GBank gjl2129478 pir S51939 - chitinase (EC 3.2.1.14) precursor - beet	UNCLASSIFIED	1004, 1029
3375	37815406 (5483, 5484)	Novel Protein sim. GBank gjl2129478 pir S51939 - chitinase (EC 3.2.1.14) precursor - beet	UNCLASSIFIED	1058
3376	79779788 (12603, 12604)	Novel Protein sim. GBank gjl2129478 pir S51939 - chitinase (EC 3.2.1.14) precursor - beet	UNCLASSIFIED	1017
3377	21144927 (18887, 18888)	Novel Protein sim. GBank gjl2129478 pir S51939 - chitinase (EC 3.2.1.14) precursor - beet	UNCLASSIFIED	1034
3378	79176240 (3543, 3544)	Novel Protein sim. GBank gjl2129582 pir S71227 - extensin 1 - Arabidopsis thaliana	UNCLASSIFIED	1001, 1024, 1037
3379	20197511 (22615, 22616)	Novel Protein sim. GBank gjl2129717 pir S71185 - ribonucleoprotein - Arabidopsis thaliana	UNCLASSIFIED	1010
3380	79968403 (13029, 13030)	Novel Protein sim. GBank gjl2129803 pir S60611 - probable serine/threonine-specific protein kinase (EC 2.7.1.-) BSK2 - rape	UNCLASSIFIED	1003
3381	80026647 (11015, 11016)	Novel Protein sim. GBank gjl2131050 emb CAB09260 - (Z95844) opcA [Mycobacterium tuberculosis]	UNCLASSIFIED	1008, 1025
3382	79241141 (6249, 6250)	Novel Protein sim. GBank gjl2131086 emb CAA89409 - (Z49389) TY4B [Saccharomyces cerevisiae]	UNCLASSIFIED	1008, 1017, 1022, 1044

3383	82361916 (17967, 17968)	Novel Protein sim. GBank gij2131212 pir S65270 - CIN2 protein - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1001, 1006, 1008, 1009, 1017, 1022, 1023, 1024, 1026, 1031
3384	79250054 (3947, 3948)	Novel Protein sim. GBank gij2131324 pir S67605 - hypothetical protein YDL070w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003, 1008, 1009, 1023, 1026, 1039, 1044
3385	78700840 (7243, 7244)	Novel Protein sim. GBank gij2131363 pir S67773 - hypothetical protein YDL214c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1017
3386	79612232 (19013, 19014)	Novel Protein sim. GBank gij2131367 pir S67786 - hypothetical protein YDL223c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006, 1024
3387	27966059 (9077, 9078)	Novel Protein sim. GBank gij2131427 pir S69784 - hypothetical protein YDR318w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1034
3388	79224048 (16343, 16344)	Novel Protein sim. GBank gij2131439 pir S70113 - hypothetical protein YDR348c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1034
3389	94127710 (9791, 9792)	Novel Protein sim. GBank gij2131522 pir S69649 - hypothetical protein YDR482c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1019
3390	27843770 (19453, 19454)	Novel Protein sim. GBank gij2131525 pir S69656 - hypothetical protein YDR489w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003, 1006
3391	79601400 (15675, 15676)	Novel Protein sim. GBank gij2131544 pir S69580 - hypothetical protein YDR524c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006
3392	80494094 (17089, 17090)	Novel Protein sim. GBank gij2131759 pir S61623 - hypothetical protein YLR049c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006, 1008, 1012, 1017, 1026, 1034, 1039, 1044
3393	80063200 (14865, 14866)	Novel Protein sim. GBank gij2131774 pir S64929 - hypothetical protein YLR095c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1022, 1024, 1039, 1044

3394	80046388 (10681, 10682)	Novel Protein sim. GBank gij2132008 pir S66765 - hypothetical protein YOL072w - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1024
3395	20699082 (22425, 22426)	Novel Protein sim. GBank gij2132050 pir S66963 - hypothetical protein YOR080w - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1006, 1022
3396	78526296 (19713, 19714)	Novel Protein sim. GBank gij2132053 pir S61651 - hypothetical protein YOR091w - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1044
3397	80171188 (9649, 9650)	Novel Protein sim. GBank gij2132079 pir S67081 - hypothetical protein YOR189w - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1026, 1058
3398	80241731 (9467, 9468)	Novel Protein sim. GBank gij2132083 pir S67089 - hypothetical protein YOR197w - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1001, 1003, 1006, 1022, 1044
3399	30664343 (5645, 5646)	Novel Protein sim. GBank gij2132143 pir S67284 - hypothetical protein YOR372c - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1022
3400	16788040 (6009, 6010)	Novel Protein sim. GBank gij2132211 pir S65168 - hypothetical protein YPL157w - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1044
3401	30658468 (17591, 17592)	Novel Protein sim. GBank gij2132221 pir S65192 - hypothetical protein YPL180w - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1026
3402	80216685 (18845, 18846)	Novel Protein sim. GBank gij2132221 pir S65192 - hypothetical protein YPL180w - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1004, 1010, 1022, 1023, 1024, 1025, 1034, 1044
3403	94655380 (10543, 10544)	Novel Protein sim. GBank gij2132225 pir S65212 - hypothetical protein YPL193w - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1022
3404	18356013 (9991, 9992)	Novel Protein sim. GBank gij2132243 pir S61028 - hypothetical protein YPL236c - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1024
3405	79415457 (1537, 1538)	Novel Protein sim. GBank gij2132244 pir S61023 - hypothetical protein YPL242c - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1006, 1022, 1026

3406	79862623 (12767, 12768)	Novel Protein sim. GBank gij2132244 pir S61023 - hypothetical protein YPL242c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1038
3407	30504759 (3089, 3090)	Novel Protein sim. GBank gij2132279 pir S69079 - hypothetical protein YPR097w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1026
3408	29683027 (1093, 1094)	Novel Protein sim. GBank gij2132286 pir S59777 - hypothetical protein YPR112c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1009
3409	78487262 (4385, 4386)	Novel Protein sim. GBank gij2132299 pir S69029 - hypothetical protein YPR140w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1009
3410	80416610 (10715, 10716)	Novel Protein sim. GBank gij2132314 pir S59832 - hypothetical protein YPR174c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1001, 1004, 1006, 1008, 1009, 1010, 1012, 1017, 1022, 1023, 1024, 1025, 1026, 1034, 1039, 1044, 1054
3411	79865587 (14455, 14456)	Novel Protein sim. GBank gij2132314 pir S59832 - hypothetical protein YPR174c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1038, 1039
3412	11691490 (13615, 13616)	Novel Protein sim. GBank gij2132443 pir S67691 - probable membrane protein YDL144c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1034
3413	30245995 (6753, 6754)	Novel Protein sim. GBank gij2132445 pir S67696 - probable membrane protein YDL148c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1026
3414	11815275 (803, 804)	Novel Protein sim. GBank gij2132492 pir S70118 - probable membrane protein YDR288w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1004

3415	77518899 (16891, 16892)	Novel Protein sim. GBank gij2132512 pir S62018 - probable membrane protein YDR539w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1011
3416	78182134 (16523, 16524)	Novel Protein sim. GBank gij2132645 pir S64754 - probable membrane protein YLL012w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1053
3417	78366762 (19485, 19486)	Novel Protein sim. GBank gij2132671 pir S61631 - probable membrane protein YLR057w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1008
3418	25316193 (21451, 21452)	Novel Protein sim. GBank gij2132671 pir S61631 - probable membrane protein YLR057w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1009
3419	80233856 (5185, 5186)	Novel Protein sim. GBank gij2132679 pir S64916 - probable membrane protein YLR084c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003, 1004, 1006, 1008, 1010, 1017, 1022, 1026, 1044
3420	27931484 (7557, 7558)	Novel Protein sim. GBank gij2132687 pir S64940 - probable membrane protein YLR104w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006, 1010, 1022
3421	8498667 (21817, 21818)	Novel Protein sim. GBank gij2132824 pir S66701 - probable membrane protein YOL019w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1034
3422	79608104 (16319, 16320)	Novel Protein sim. GBank gij2132845 pir S66802 - probable membrane protein YOL106w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1025
3423	16820311 (17299, 17300)	Novel Protein sim. GBank gij2132852 pir S66835 - probable membrane protein YOL138c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1017

3424	17938485 (3097, 3098)	Novel Protein sim. GBank gj 2132868 pir S66936 - probable membrane protein YOR053w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1039
3425	10198761 (13353, 13354)	Novel Protein sim. GBank gj 2132879 pir S61647 - probable membrane protein YOR086c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003
3426	25335616 (3657, 3658)	Novel Protein sim. GBank gj 2132889 pir S61667 - probable membrane protein YOR109w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1008
3427	20416759 (14391, 14392)	Novel Protein sim. GBank gj 2132900 pir S67042 - probable membrane protein YOR154w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1004
3428	80234470 (4007, 4008)	Novel Protein sim. GBank gj 2132906 pir S67067 - probable membrane protein YOR175c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1004, 1022, 1023
3429	57530356 (1241, 1242)	Novel Protein sim. GBank gj 2132917 pir S60941 - probable membrane protein YOR214c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1004, 1006, 1008, 1010, 1012, 1022, 1024, 1034, 1039, 1044
3430	27779527 (15327, 15328)	Novel Protein sim. GBank gj 2132940 pir S67203 - probable membrane protein YOR299w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1022, 1024
3431	13526994 (117, 118)	Novel Protein sim. GBank gj 2132946 pir S58330 - probable membrane protein YOR320c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1024
3432	27788823 (13705, 13706)	Novel Protein sim. GBank gj 2132947 pir S58333 - probable membrane protein YOR322c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1022, 1024

3433	79452038 (19017, 19018)	Novel Protein sim. GBank gi 2133004 pir S65240 - probable membrane protein YPL221w - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1003, 1008, 1017, 1022, 1023, 1026, 1039
3434	80232215 (323, 324)	Novel Protein sim. GBank gi 2133040 pir S59842 - probable membrane protein YPR185w - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1004, 1008, 1010, 1024
3435	79451977 (4539, 4540)	Novel Protein sim. GBank gi 2133040 pir S59842 - probable membrane protein YPR185w - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1022
3436	20428628 (13727, 13728)	Novel Protein sim. GBank gi 2134419 pir A57075 - tensin - chicken (fragment)	UNCLASSIFIED	1010, 1022
3437	65661259 (1723, 1724)	Novel Protein sim. GBank gi 2135416 pir 38022 - hypothetical protein - human	UNCLASSIFIED	1041
3438	19648067 (5517, 5518)	Novel Protein sim. GBank gi 2135416 pir 38022 - hypothetical protein - human	UNCLASSIFIED	1017, 1023
3439	20721495 (15509, 15510)	Novel Protein sim. GBank gi 2135950 pir S58222 - PQ-rich protein - human	UNCLASSIFIED	1006
3440	9945274 (11321, 11322)	Novel Protein sim. GBank gi 2137043 pir 46880 - unknown protein - rabbit (fragment)	UNCLASSIFIED	1044
3441	20430944 (3251, 3252)	Novel Protein sim. GBank gi 2137044 pir 46884 - unknown protein - rabbit (fragment)	UNCLASSIFIED	1024
3442	13518144 (9975, 9976)	Novel Protein sim. GBank gi 2137044 pir 46884 - unknown protein - rabbit (fragment)	UNCLASSIFIED	1024
3443	95199127 (10471, 10472)	Novel Protein sim. GBank gi 2137044 pir 46884 - unknown protein - rabbit (fragment)	UNCLASSIFIED	1029

3444	27956156 (5923, 5924)	Novel Protein sim. GBank gjl2137729 pir 60167 - regulatory protein Nedd1 - mouse	UNCLASSIFIED	1004
3445	86380882 (4425, 4426)	Novel Protein sim. GBank gjl2143780 pir 56545 - heparan sulfate proteoglycan - rat	UNCLASSIFIED	1053
3446	65876808 (81, 82)	Novel Protein sim. GBank gjl2144041 pir 56505 - protein-L-isoaspartate(D-aspartate) O-methyltransferase (EC 2.1.1.77) - black rat	UNCLASSIFIED	1044
3447	17899265 (17521, 17522)	Novel Protein sim. GBank gjl2144188 pir JC4743 - fatty-acid synthase (EC 2.3.1.85) - Mycobacterium tuberculosis	UNCLASSIFIED	1044
3448	20625052 (5131, 5132)	Novel Protein sim. GBank gjl2145947 pir S72959 - probable integrase - Mycobacterium leprae	UNCLASSIFIED	1010
3449	79861915 (4431, 4432)	Novel Protein sim. GBank gjl2145957 pir S72983 - probable phosphorylating protein ureC - Mycobacterium leprae	UNCLASSIFIED	1012
3450	27843590 (345, 346)	Novel Protein sim. GBank gjl2146828 pir S74288 - hypothetical protein YCL008c - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1022
3451	78795977 (22439, 22440)	Novel Protein sim. GBank gjl2147083 pir S88957 - adhesive protein - Mytilus galloprovincialis	UNCLASSIFIED	1026
3452	80503574 (13333, 13334)	Novel Protein sim. GBank gjl2181957 emb CAB09445 - (Z96070) hypothetical protein Rv3300c [Mycobacterium tuberculosis]	UNCLASSIFIED	1012
3453	17938994 (15779, 15780)	Novel Protein sim. GBank gjl2182006 emb CAB09475 - (Z96072) hypothetical protein Rv2715 [Mycobacterium tuberculosis]	UNCLASSIFIED	1038
3454	25262844 (1791, 1792)	Novel Protein sim. GBank gjl2183273 (AF002133) - MAV266 [Mycobacterium avium]	UNCLASSIFIED	1009

3455	20446782 (8021, 8022)	Novel Protein sim. GBank gi 2190951 (AF002247) - transposase [Rhodococcus erythropolis]		UNCLASSIFIED	1024
3456	11091074 (19113, 19114)	Novel Protein sim. GBank gi 2190953 (AF002247) - ORF2 [Rhodococcus erythropolis]		UNCLASSIFIED	1006
3457	15015721 (1079, 1080)	Novel Protein sim. GBank gi 2193870 dbj BAA20419 - (D84391) reverse transcriptase [Mus musculus]		UNCLASSIFIED	1001
3458	99327112 (4143, 4144)	Novel Protein sim. GBank gi 2193870 dbj BAA20419 - (D84391) reverse transcriptase [Mus musculus]		UNCLASSIFIED	1006, 1010, 1016, 1017, 1022, 1023, 1024, 1029, 1034, 1038, 1039
3459	34129286 (16021, 16022)	Novel Protein sim. GBank gi 2193870 dbj BAA20419 - (D84391) reverse transcriptase [Mus musculus]		UNCLASSIFIED	1026
3460	79206061 (22517, 22518)	Novel Protein sim. GBank gi 2193870 dbj BAA20419 - (D84391) reverse transcriptase [Mus musculus]		UNCLASSIFIED	1034
3461	57143751 (14417, 14418)	Novel Protein sim. GBank gi 2197106 (AF003693) - scaffold protein Pbp1 homolog [Mus musculus]		UNCLASSIFIED	1022, 1034, 1058
3462	78471189 (13205, 13206)	Novel Protein sim. GBank gi 2204224 emb CAA74161 - (Y13849) alpha-galactosidase [Hordeum vulgare]		UNCLASSIFIED	1053
3463	13502091 (20483, 20484)	Novel Protein sim. GBank gi 2213527 emb CAB09730 - (Z97050) hypothetical protein Rv0190 [Mycobacterium tuberculosis]		UNCLASSIFIED	1027
3464	80048915 (8137, 8138)	Novel Protein sim. GBank gi 2216156 (AF005091) - lipase/esterase; EstA [Pseudomonas aeruginosa]		UNCLASSIFIED	1034
3465	30621011 (12939, 12940)	Novel Protein sim. GBank gi 2224529 dbj BAA20754 - (AB002292) KIAA0294 [Homo sapiens]		UNCLASSIFIED	1026

3466	27966891 (1313, 1314)	Novel Protein sim. GBank gi 2224589 dbj BAA20782 - (AB002322) KIAA0324 [Homo sapiens]	UNCLASSIFIED	1006
3467	56713726 (4267, 4268)	Novel Protein sim. GBank gi 2225877 dbj BAA20875.1 - (AB002406) TIP49 [Rattus norvegicus]	UNCLASSIFIED	1016
3468	20700807 (20953, 20954)	Novel Protein sim. GBank gi 2225941 emb CAA69714 - (Y08460) Mdes protein [Mus musculus]	UNCLASSIFIED	1022, 1034
3469	37374805 (10051, 10052)	Novel Protein sim. GBank gi 2226204 emb CAA74493.1 - (Y14082) hypothetical protein [Bacillus subtilis]	UNCLASSIFIED	1023
3470	79553182 (12831, 12832)	Novel Protein sim. GBank gi 2226238 emb CAA74526.1 - (Y14083) hypothetical protein [Bacillus subtilis]	UNCLASSIFIED	1039
3471	80026633 (9661, 9662)	Novel Protein sim. GBank gi 2226243 emb CAA74531.1 - (Y14083) hypothetical protein [Bacillus subtilis]	UNCLASSIFIED	1006
3472	77516818 (20355, 20356)	Novel Protein sim. GBank gi 2226283 (U70053) - GumP [Xanthomonas campestris]	UNCLASSIFIED	1049
3473	29247926 (7377, 7378)	Novel Protein sim. GBank gi 2239236 emb CAB10154 - (Z97211) probable involvement in ergosterol synthesis [Schizosaccharomyces pombe]	UNCLASSIFIED	1022
3474	21425340 (3577, 3578)	Novel Protein sim. GBank gi 2244627 dbj BAA21097 - (D89876) hemolysin [Edwardsiella tarda]	UNCLASSIFIED	1053
3475	36999858 (11821, 11822)	Novel Protein sim. GBank gi 2253084 emb CAA74602 - (Y14206) orfsyn [Streptomyces coelicolor]	UNCLASSIFIED	1001
3476	23308531 (14629, 14630)	Novel Protein sim. GBank gi 2262102 gb AAB63610.1 - (AC002343) hypothetical protein [Arabidopsis thaliana]	UNCLASSIFIED	1053
3477	78620830 (11081, 11082)	Novel Protein sim. GBank gi 226591 prt 1603238B - ATP synthase 18kD-like protein 4 [Saccharomycetales]	UNCLASSIFIED	1009

3478	20739345 (3283, 3284)	Novel Protein sim. GBank gil226743 prf 1604369A - sulfated surface glycoprotein SSG185 [Volvox carter]		UNCLASSIFIED	1022
3479	36986952 (8143, 8144)	Novel Protein sim. GBank gil2270983 (U0220) - orf3 [Sinorhizobium meliloti]		UNCLASSIFIED	1001
3480	2333109 (4883, 4884)	Novel Protein sim. GBank gil2275199 (AC002337) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	1053
3481	8498660 (21299, 21300)	Novel Protein sim. GBank gil2276127 dbj BAA21556 - (D88585) hepatitis A virus receptor [Chlorocebus aethiops]		UNCLASSIFIED	1024
3482	11817991 (21249, 21250)	Novel Protein sim. GBank gil2276392 (U02634) - Dxr/iron regulated protein 2 [Corynebacterium diphtheriae]		UNCLASSIFIED	1004
3483	30750523 (18449, 18450)	Novel Protein sim. GBank gil2282048 (AF009900) - ZZ3 protein [Vibrio shiloi]		UNCLASSIFIED	1023
3484	9857085 (15293, 15294)	Novel Protein sim. GBank gil2288879 emb CAA71776 - (Y10817) molybdate binding periplasmic protein [Arthrobacter nicotinovorans]		UNCLASSIFIED	1008
3485	37032756 (7041, 7042)	Novel Protein sim. GBank gil2290990 (AF006000) - Brg1 [Bordetella pertussis]		UNCLASSIFIED	1038
3486	37028591 (15467, 15468)	Novel Protein sim. GBank gil2290990 (AF006000) - Brg1 [Bordetella pertussis]		UNCLASSIFIED	1038
3487	13076276 (5581, 5582)	Novel Protein sim. GBank gil2292957 emb CAB10899 - (Z98209) hypothetical protein Rv2723 [Mycobacterium tuberculosis]		UNCLASSIFIED	1031
3488	27981617 (14005, 14006)	Novel Protein sim. GBank gil2292959 emb CAB10901 - (Z98209) hflX [Mycobacterium tuberculosis]		UNCLASSIFIED	1006
3489	29518763 (2949, 2950)	Novel Protein sim. GBank gil2293166 (AF008220) - amino acid transporter [Bacillus subtilis]		UNCLASSIFIED	1016
3490	78760837 (1991, 1992)	Novel Protein sim. GBank gil2293167 (AF008220) - probable lysophospholipase [Bacillus subtilis]		UNCLASSIFIED	1003

3491	11289499 (18353, 18354)	Novel Protein sim. GBank gi 2293174 (AF008220) - YtrF [Bacillus subtilis]	UNCLASSIFIED	1022
3492	78675833 (21063, 21064)	Novel Protein sim. GBank gi 2293568 (AF012897) - Hvb12D homolog [Oryza sativa]	UNCLASSIFIED	1017
3493	13886343 (4129, 4130)	Novel Protein sim. GBank gi 2313702(gb)/AAD07650.1] - (AE000571) H. pylori predicted coding region HP0578 [Helicobacter pylori 26695]	UNCLASSIFIED	1053
3494	79247119 (12493, 12494)	Novel Protein sim. GBank gi 2314191(gb)/AAD08089.1] - (AE000612) conserved hypothetical integral membrane protein [Helicobacter pylori 26695]	UNCLASSIFIED	1038
3495	80209505 (15055, 15056)	Novel Protein sim. GBank gi 2314238(gb)/AAD08133.1] - (AE000615) H. pylori predicted coding region HP1081 [Helicobacter pylori 26695]	UNCLASSIFIED	1034
3496	13883844 (16667, 16668)	Novel Protein sim. GBank gi 2314367(gb)/AAD08251.1] - (AE000626) multidrug resistance protein (hetA) [Helicobacter pylori 26695]	UNCLASSIFIED	1053
3497	8975576 (3615, 3616)	Novel Protein sim. GBank gi 231481(sp)/P29958 AAC_ACTUT - ACULEACIN A ACYLASE PRECURSOR	UNCLASSIFIED	1017
3498	20634331 (17073, 17074)	Novel Protein sim. GBank gi 2317934 (U97553) - unknown [murine herpesvirus 68]	UNCLASSIFIED	1004
3499	21417200 (16249, 16250)	Novel Protein sim. GBank gi 232042(sp)/P29541 EFG_STRRA - ELONGATION FACTOR G (EF-G)	UNCLASSIFIED	1022
3500	20282053 (6479, 6480)	Novel Protein sim. GBank gi 2326732(emb)/CAB10946] - (Z98268) tyrS [Mycobacterium tuberculosis]	UNCLASSIFIED	1022
3501	11347016 (17377, 17378)	Novel Protein sim. GBank gi 2326732(emb)/CAB10946] - (Z98268) tyrS [Mycobacterium tuberculosis]	UNCLASSIFIED	1034
3502	80050108 (19247, 19248)	Novel Protein sim. GBank gi 2326739(emb)/CAB10953] - (Z98268) recN [Mycobacterium tuberculosis]	UNCLASSIFIED	1004, 1006, 1022, 1044

3503	79825231 (2713, 2714)	Novel Protein sim. GBank gi 2326740 emb CAB10954 - (Z98268) hypothetical protein Rv1697 [Mycobacterium tuberculosis]	UNCLASSIFIED	1039
3504	80092742 (6719, 6720)	Novel Protein sim. GBank gi 2330641 emb CAA74897 - (Y14568) htrB [Pseudomonas fluorescens]	UNCLASSIFIED	1006
3505	80239603 (18457, 18458)	Novel Protein sim. GBank gi 2330791 emb CAB11265 - (Z98601) carboxypeptidase s precursor [Schizosaccharomyces pombe]	UNCLASSIFIED	1004, 1010
3506	20288157 (1181, 1182)	Novel Protein sim. GBank gi 2337823 emb CAB11300 - (Z98604) hypothetical protein MLCB2052.02 [Mycobacterium leprae]	UNCLASSIFIED	1034
3507	85800430 (9741, 9742)	Novel Protein sim. GBank gi 2337836 emb CAB11328 - (Z98604) ABC-type sugar transport protein [Mycobacterium leprae]	UNCLASSIFIED	1025
3508	23302830 (9383, 9384)	Novel Protein sim. GBank gi 2340008 emb CAB11358 - (Z98682) Y1bL protein [Bacillus subtilis]	UNCLASSIFIED	1008
3509	79249087 (19971, 19972)	Novel Protein sim. GBank gi 2342605 emb CAB11373 - (Z98741) nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase [Mycobacterium leprae]	UNCLASSIFIED	1024, 1044
3510	11751284 (1269, 1270)	Novel Protein sim. GBank gi 2343283 (AF015297) - IE2hom [Human herpesvirus 6 (strain Uganda-1102)]	UNCLASSIFIED	1022
3511	80170492 (9687, 9688)	Novel Protein sim. GBank gi 2347197 (AC002338) - hypothetical protein [Arabidopsis thaliana]	UNCLASSIFIED	1008, 1058
3512	70074365 (5251, 5252)	Novel Protein sim. GBank gi 2351772 (U90267) - p39 [Mus musculus]	UNCLASSIFIED	1042

3513	27365977 (15743, 15744)	Novel Protein sim. GBank gij2352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Oryctolagus cuniculus]		UNCLASSIFIED	1022
3514	9666959 (19727, 19728)	Novel Protein sim. GBank gij2370322[emb]CAB11595] - (Z98943) hypothetical protein Rv1533 [Mycobacterium tuberculosis]		UNCLASSIFIED	1023
3515	20485309 (9979, 9980)	Novel Protein sim. GBank gij2384728[gb]AAB69862.1] - (AF015883) hydroxyproline-rich glycoprotein gas28p precursor [Chlamydomonas reinhardtii]		UNCLASSIFIED	1022
3516	94140178 (5271, 5272)	Novel Protein sim. GBank gij2388988[emb]CAB11718] - (Z98980) actin associated protein [Schizosaccharomyces pombe]		UNCLASSIFIED	1003, 1010, 1018, 1023, 1038, 1049, 1054
3517	11091025 (13033, 13034)	Novel Protein sim. GBank gij2398792[emb]CAA60713] - (X87256) glutamine amidotransferase [Rhodobacter sphaeroides]		UNCLASSIFIED	1006
3518	19888230 (13891, 13892)	Novel Protein sim. GBank gij2407197 (AF017138) - cob(I)alamin adenosyltransferase [Rhodobacter capsulatus]		UNCLASSIFIED	1034
3519	95005613 (12071, 12072)	Novel Protein sim. GBank gij2414562[emb]CAB16451] - (Z99263) polyphosphate kinase [Mycobacterium leprae]		UNCLASSIFIED	1034
3520	13085228 (20019, 20020)	Novel Protein sim. GBank gij2415403 (AF015775) - acetylornithine deacetylase [Bacillus subtilis]		UNCLASSIFIED	1027
3521	9383239 (3637, 3638)	Novel Protein sim. GBank gij2415704[emb]CAA04698] - (AJ001361) proline iminopeptidase [Propionibacterium freudenreichii subsp. shermanii]		UNCLASSIFIED	1017
3522	10886132 (4323, 4324)	Novel Protein sim. GBank gij2435511 (AF024504) - contains similarity to prolyl 4-hydroxylase alpha subunit [Arabidopsis thaliana]		UNCLASSIFIED	1031

3523	78936412 (8079, 8080)	Novel Protein sim. GBank gij2435511 (AF024504) - contains similarity to polyI 4-hydroxylase alpha subunit [Arabidopsis thaliana]	UNCLASSIFIED	1008, 1044
3524	20616812 (13419, 13420)	Novel Protein sim. GBank gij2440103[emb]CAB16676] - (Z99494) hypothetical protein MLCB57.36c [Mycobacterium leprae]	UNCLASSIFIED	1010
3525	27969777 (18557, 18558)	Novel Protein sim. GBank gij2444466 (AF021840) - AldA [Ralstonia solanacearum]	UNCLASSIFIED	1022
3526	52563565 (16179, 16180)	Novel Protein sim. GBank gij2477513 (AC002398) - F25965_3 [Homo sapiens]	UNCLASSIFIED	1039
3527	11706954 (19055, 19056)	Novel Protein sim. GBank gij2492593[sp]P55604[Y4OS_RHISN - PROBABLE ABC TRANSPORTER ATP-BINDING PROTEIN Y4OS	UNCLASSIFIED	1022
3528	56288155 (6989, 6990)	Novel Protein sim. GBank gij2493240[sp]O10341[Y091_NPVOP - HYPOTHETICAL 29.3 KD PROTEIN (ORF92)	UNCLASSIFIED	1037, 1038
3529	39581745 (15797, 15798)	Novel Protein sim. GBank gij2493240[sp]O10341[Y091_NPVOP - HYPOTHETICAL 29.3 KD PROTEIN (ORF92)	UNCLASSIFIED	1038
3530	79637559 (2301, 2302)	Novel Protein sim. GBank gij2494014[sp]Q59967[SRPH_SYNPF7 - SERINE ACETYLTRANSFERASE, PLASMID (SAT)	UNCLASSIFIED	1006, 1038
3531	80051091 (9435, 9436)	Novel Protein sim. GBank gij2494531[sp]P75938[FLGF_ECOLI - FLAGELLAR BASAL-BODY ROD PROTEIN FLGF (PUTATIVE PROXIMAL ROD PROTEIN)	UNCLASSIFIED	1004
3532	32153325 (17829, 17830)	Novel Protein sim. GBank gij2494538[sp]Q52950[FLGH_RHIME - FLAGELLAR L-RING PROTEIN PRECURSOR (BASAL BODY L-RING PROTEIN)	UNCLASSIFIED	1023

3533	86380254 (4415, 4416)	Novel Protein sim. GBank gil2494630 sp Q64467 G3PT_MOUSE - GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, TESTIS-SPECIFIC (GAPDH)		UNCLASSIFIED	1053
3534	20724433 (15979, 15980)	Novel Protein sim. GBank gil2495381 sp P77300 YAGL_ECOLI - HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN PERR-ARGF INTERGENIC REGION		UNCLASSIFIED	1006
3535	12917471 (9881, 9882)	Novel Protein sim. GBank gil2495562 sp P77239 YLCD_ECOLI - HYPOTHETICAL 44.3 KD PROTEIN IN NFRB- PHEP INTERGENIC REGION PRECURSOR		UNCLASSIFIED	1004
3536	27972911 (18581, 18582)	Novel Protein sim. GBank gil2495572 sp P75744 YBGJ_ECOLI - HYPOTHETICAL 23.9 KD PROTEIN IN PHRB- NEL INTERGENIC REGION		UNCLASSIFIED	1053
3537	11777222 (15459, 15460)	Novel Protein sim. GBank gil2495597 sp P77334 YCIIR_ECOLI - HYPOTHETICAL 74.7 KD PROTEIN IN OSMB- RNB INTERGENIC REGION		UNCLASSIFIED	1022
3538	80248157 (16699, 16700)	Novel Protein sim. GBank gil2495634 sp P76518 YFDE_ECOLI - HYPOTHETICAL 43.3 KD PROTEIN IN EVGS- GLK INTERGENIC REGION		UNCLASSIFIED	1003, 1006
3539	79872214 (3367, 3368)	Novel Protein sim. GBank gil2495648 sp P76562 YPF1_ECOLI - HYPOTHETICAL 74.9 KD PROTEIN IN DAPE- PURC INTERGENIC REGION		UNCLASSIFIED	1017
3540	20514013 (14781, 14782)	Novel Protein sim. GBank gil2495651 sp P55734 YGAP_ECOLI - HYPOTHETICAL 18.6 KD PROTEIN IN GABP- STPA INTERGENIC REGION		UNCLASSIFIED	1010
3541	11130950 (7313, 7314)	Novel Protein sim. GBank gil2495685 sp Q57498 YA53_HAEIN - HYPOTHETICAL PROTEIN HI1053		UNCLASSIFIED	1004

3542	27794695 (15277, 15278)	Novel Protein sim. GBank gil2495701 sp Q14135 Y121_HUMAN - HYPOTHETICAL PROTEIN KIAA0121	UNCLASSIFIED	1024
3543	78377579 (2521, 2522)	Novel Protein sim. GBank gil2496136 sp Q58288 Y878_METJA - HYPOTHETICAL PROTEIN MJ0878	UNCLASSIFIED	1008, 1016, 1026
3544	80248456 (1931, 1932)	Novel Protein sim. GBank gil2496481 sp Q50724 Y09S_MYCTU - HYPOTHETICAL 87.3 KD PROTEIN CY78.27C	UNCLASSIFIED	1006, 1010, 1022, 1023, 1024, 1026, 1031, 1034, 1039
3545	78461809 (2507, 2508)	Novel Protein sim. GBank gil2496484 sp Q49741 Y09T_MYCLE - HYPOTHETICAL 28.6 KD PROTEIN B1620_F3_119	UNCLASSIFIED	1023, 1049
3546	78490684 (6681, 6682)	Novel Protein sim. GBank gil2496491 sp Q50739 Y0A9_MYCTU - HYPOTHETICAL 47.5 KD PROTEIN CY9C4.09	UNCLASSIFIED	1030
3547	79641125 (21033, 21034)	Novel Protein sim. GBank gil2496533 sp Q50598 Y0D8_MYCTU - HYPOTHETICAL 69.9 KD PROTEIN CY1A11.08	UNCLASSIFIED	1039
3548	11360207 (2209, 2210)	Novel Protein sim. GBank gil2496621 sp P55441 Y4FC_RHISN - HYPOTHETICAL MONOOXYGENASE Y4FC	UNCLASSIFIED	1006
3549	80081058 (19623, 19624)	Novel Protein sim. GBank gil2496798 sp P74311 Y944_SYNY3 - HYPOTHETICAL 42.4 KD PROTEIN SLR0944	UNCLASSIFIED	1017, 1034
3550	66137941 (20945, 20946)	Novel Protein sim. GBank gil2496862 sp Q11116 YX0A_CAEEL - HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X	UNCLASSIFIED	1003
3551	8488862 (21215, 21216)	Novel Protein sim. GBank gil2497058 sp Q03102 YMN1_YEAST - HYPOTHETICAL 40.0 KD PROTEIN IN COX14 5'REGION	UNCLASSIFIED	1022

3552	27838700 (22901, 22902)	Novel Protein sim. GBank gij2497061 sp Q03124 YMM7_YEAST - HYPOTHETICAL 65.2 KD PROTEIN IN COX14- HMGS INTERGENIC REGION		UNCLASSIFIED	1004, 1006, 1010, 1022, 1034
3553	80221866 (6975, 6976)	Novel Protein sim. GBank gij2497090 sp Q04693 YME9_YEAST - HYPOTHETICAL 153.8 KD PROTEIN IN GAL80- PRP39 INTERGENIC REGION		UNCLASSIFIED	1004, 1006, 1009, 1010, 1012, 1016, 1023, 1024, 1034, 1038, 1044
3554	80233217 (14689, 14690)	Novel Protein sim. GBank gij2497090 sp Q04693 YME9_YEAST - HYPOTHETICAL 153.8 KD PROTEIN IN GAL80- PRP39 INTERGENIC REGION		UNCLASSIFIED	1004, 1006, 1009, 1010, 1016, 1017, 1022, 1025, 1026, 1038, 1039
3555	32124806 (20505, 20506)	Novel Protein sim. GBank gij2497099 sp Q03712 YMD3_YEAST - HYPOTHETICAL 17.7 KD PROTEIN IN AMD1- RAD52 INTERGENIC REGION		UNCLASSIFIED	1003, 1004, 1006, 1009, 1012, 1017, 1022, 1038, 1044
3556	28987444 (22625, 22626)	Novel Protein sim. GBank gij2497112 sp Q03667 YMO2_YEAST - HYPOTHETICAL 16.7 KD PROTEIN IN CDC5- MVP1 INTERGENIC REGION		UNCLASSIFIED	1023, 1024
3557	5641214 (17489, 17490)	Novel Protein sim. GBank gij2497143 sp Q04279 YMX6_YEAST - HYPOTHETICAL 105.9 KD PROTEIN IN ADH3- RCA1 INTERGENIC REGION		UNCLASSIFIED	1058
3558	78729015 (19393, 19394)	Novel Protein sim. GBank gij2497148 sp Q03153 YMY8_YEAST - HYPOTHETICAL 70.4 KD PROTEIN IN SNZ1- YPK2 INTERGENIC REGION		UNCLASSIFIED	1008
3559	80218584 (2733, 2734)	Novel Protein sim. GBank gij2497157 sp Q03879 YMO9_YEAST - VERY HYPOTHETICAL 14.1 KD PROTEIN IN RPL108- GCR3 INTERGENIC REGION		UNCLASSIFIED	1003, 1022

3560	78971625 (7787, 7788)	Novel Protein sim. GBank gij2497217 sp Q03264 YM80_YEAST - HYPOTHETICAL 59.5 KD PROTEIN IN HDF1- MRPL33 INTERGENIC REGION		UNCLASSIFIED	1017
3561	29346175 (17229, 17230)	Novel Protein sim. GBank gij2497226 sp Q04869 YM94_YEAST - HYPOTHETICAL 38.2 KD PROTEIN IN PRE5- FET4 INTERGENIC REGION		UNCLASSIFIED	1022
3562	5715218 (867, 868)	Novel Protein sim. GBank gij2497227 sp Q04893 YM96_YEAST - HYPOTHETICAL 113.1 KD PROTEIN IN PRE5- FET4 INTERGENIC REGION		UNCLASSIFIED	1058
3563	79821196 (11795, 11796)	Novel Protein sim. GBank gij2497384 sp Q46087 TRAT_CHEHE - TRANSPPOSASE		UNCLASSIFIED	1039
3564	20399484 (6139, 6140)	Novel Protein sim. GBank gij2497419 sp P55635 Y4RB_RHISN - PUTATIVE INTEGRASE/RECOMBINASE Y4RB		UNCLASSIFIED	1004
3565	14218558 (6293, 6294)	Novel Protein sim. GBank gij2497717 sp P55969 HPA0_HELPY - NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ PRECURSOR (N- ACETYLNEURAMINYLLACTOSE-BINDING FIBRILLAR HEMAGGLUTININ RECEPTOR- BINDING SUBUNIT) (NLBH) (FLAGELLAR SHEATH ADHESIN)		UNCLASSIFIED	1053
3566	78461564 (9069, 9070)	Novel Protein sim. GBank gij2498270 sp Q02554 CUS1_YEAST - CUS1 PROTEIN		UNCLASSIFIED	1006, 1044
3567	21145908 (16663, 16664)	Novel Protein sim. GBank gij2499125 sp Q07878 VP13_YEAST - VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13		UNCLASSIFIED	1058

3568	80190320 (18657, 18658)	Novel Protein sim. GBank gi 2499125 sp Q07878 VP13_YEAST - VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13		UNCLASSIFIED	1058
3569	16332986 (13881, 13882)	Novel Protein sim. GBank gi 2499516 sp Q57290 Y740_HAEIN - PROBABLE PHOSPHOMANNOMUTASE (PMM)		UNCLASSIFIED	1024
3570	12936190 (15989, 15990)	Novel Protein sim. GBank gi 2500021 sp Q46480 PUR9_CHRVI - PHOSPHORIBOSYLAMINOIMIDAZOLECARBOX AMIDE FORMYLTRANSFERASE (AICAR TRANSFORMYLASE) / IMP CYCLOHYDROLASE (INOSINICASE) (IMP SYNTHETASE) (ATIC)		UNCLASSIFIED	1004
3571	27972399 (12581, 12582)	Novel Protein sim. GBank gi 2500034 sp P72170 PYRC_PSEAE - DIHYDROOROTASE (DHOASE)		UNCLASSIFIED	1022
3572	80054174 (10931, 10932)	Novel Protein sim. GBank gi 2500056 sp Q46267 PFLA_CLOPA - PYRUVATE FORMATE-LYASE ACTIVATING ENZYME		UNCLASSIFIED	1004
3573	20726654 (13265, 13266)	Novel Protein sim. GBank gi 2500056 sp Q46267 PFLA_CLOPA - PYRUVATE FORMATE-LYASE ACTIVATING ENZYME		UNCLASSIFIED	1006
3574	11102137 (5021, 5022)	Novel Protein sim. GBank gi 25000728 sp Q59912 SECY_STRGB - PREPROTEIN TRANSLOCASE SECY SUBUNIT		UNCLASSIFIED	1006
3575	77600954 (21265, 21266)	Novel Protein sim. GBank gi 2500739 sp Q51455 CHEY_PSEAE - CHEMOTAXIS PROTEIN CHEY		UNCLASSIFIED	1049
3576	78674817 (14837, 14838)	Novel Protein sim. GBank gi 2500772 sp Q07657 YD25_YEAST - HYPOTHETICAL 62.6 KD PROTEIN IN CDC13- GCS1 INTERGENIC REGION		UNCLASSIFIED	1017

3577	11392472 (10613, 10614)	Novel Protein sim. GBank gi 2500995 sp Q55690 SYGB_SYNY3 - GLYCYL-TRNA SYNTHETASE BETA CHAIN (GLYCINE--TRNA LIGASE BETA CHAIN) (GLYRS)	UNCLASSIFIED	1024
3578	20263972 (1027, 1028)	Novel Protein sim. GBank gi 2501000 sp Q50641 SYH_MYCTU - HISTIDYL-TRNA SYNTHETASE (HISTIDINE--TRNA LIGASE) (HISRS)	UNCLASSIFIED	1034
3579	79631866 (995, 996)	Novel Protein sim. GBank gi 2501027 sp P71698 SYL_MYCTU - LEUCYL-TRNA SYNTHETASE (LEUCINE--TRNA LIGASE) (LEURS)	UNCLASSIFIED	1039
3580	25321667 (18609, 18610)	Novel Protein sim. GBank gi 2501040 sp O05814 SYP_MYCTU - PROLYL-TRNA SYNTHETASE (PROLINE--TRNA LIGASE) (PRORS)	UNCLASSIFIED	1008
3581	27837378 (10319, 10320)	Novel Protein sim. GBank gi 2501048 sp Q55486 SYR_SYNY3 - ARGINYL-TRNA SYNTHETASE (ARGININE--TRNA LIGASE) (ARGRS)	UNCLASSIFIED	1024, 1034
3582	80050861 (7189, 7190)	Novel Protein sim. GBank gi 2501051 sp Q05506 SYRC_YEAST - PROBABLE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (ARGININE--TRNA LIGASE) (ARGRS)	UNCLASSIFIED	1034
3583	11759455 (22289, 22290)	Novel Protein sim. GBank gi 2501062 sp Q55806 SYT_SYNY3 - THREONYL-TRNA SYNTHETASE (THREONINE--TRNA LIGASE) (THRRS)	UNCLASSIFIED	1024
3584	91213847 (15803, 15804)	Novel Protein sim. GBank gi 2501068 sp Q58413 SYV_METJA - VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS)	UNCLASSIFIED	1008, 1024, 1029

3585	20451598 (12643, 12644)	Novel Protein sim. GBank gil2501069 sp Q46127 SYW_CLOLO - TRYPTOPHANYL-TRNA SYNTHETASE (TRYPTOPHAN-TRNA LIGASE) (TRPRS)	UNCLASSIFIED	1024
3586	80049352 (22959, 22960)	Novel Protein sim. GBank gil2501071 sp Q49901 SYW_MYCLE - TRYPTOPHANYL-TRNA SYNTHETASE (TRYPTOPHAN-TRNA LIGASE) (TRPRS)	UNCLASSIFIED	1010, 1024
3587	79411738 (3153, 3154)	Novel Protein sim. GBank gil2501437 sp Q06624 RH31_YEAST - DNA DAMAGE TOLERANCE PROTEIN RHC31 (RAD31 HOMOLOG)	UNCLASSIFIED	1010
3588	25259471 (9337, 9338)	Novel Protein sim. GBank gil2501527 sp P77338 AEFA_ECOLI - AEFA PROTEIN	UNCLASSIFIED	1008, 1017
3589	94141264 (21, 22)	Novel Protein sim. GBank gil2501557 sp Q47679 YAFV_ECOLI - HYPOTHETICAL 28.9 KD PROTEIN IN DNAQ- GIMHA INTERGENIC REGION	UNCLASSIFIED	1010
3590	27847764 (11175, 11176)	Novel Protein sim. GBank gil2501612 sp Q08960 YP07_YEAST - HYPOTHETICAL 89.8 KD PROTEIN YPL207W	UNCLASSIFIED	1010
3591	78678606 (7485, 7486)	Novel Protein sim. GBank gil2501652 sp Q47155 DINP_ECOLI - DNA- DAMAGE-INDUCIBLE PROTEIN P	UNCLASSIFIED	1017
3592	37034484 (22781, 22782)	Novel Protein sim. GBank gil2501679 sp Q45826 YMDA_CHLAU - HYPOTHETICAL PROTEIN IN MDH 5'REGION (ORFA)	UNCLASSIFIED	1012
3593	81815561 (12125, 12126)	Novel Protein sim. GBank gil2506592 sp P4568 DXR_ECOLI - 1-DEOXY-D- XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE (DXP REDUCTOISOMERASE)	UNCLASSIFIED	1054

3594	79769352 (14307, 14308)	Novel Protein sim. GBank gil2506652 sp P45576 YICIM_ECOLI - HYPOTHETICAL 44.5 KD PROTEIN IN PGPB- PYRF INTERGENIC REGION PRECURSOR		UNCLASSIFIED	1010, 1023
3595	78913745 (8093, 8094)	Novel Protein sim. GBank gil2506664 sp P40120 YDCG_ECOLI - 59.4 PROTEIN IN TRG-RIML INTERGENIC REGION PRECURSOR		UNCLASSIFIED	1039
3596	20747431 (12545, 12546)	Novel Protein sim. GBank gil2506664 sp P40120 YDCG_ECOLI - 59.4 PROTEIN IN TRG-RIML INTERGENIC REGION PRECURSOR		UNCLASSIFIED	1022
3597	20433662 (15745, 15746)	Novel Protein sim. GBank gil2506668 sp P31122 YDEA_ECOLI - HYPOTHETICAL 42.5 KD PROTEIN IN UXAB- MARR INTERGENIC REGION		UNCLASSIFIED	1024
3598	79239991 (8229, 8230)	Novel Protein sim. GBank gil2506685 sp P38097 YEGE_ECOLI - HYPOTHETICAL 123.9 KD PROTEIN IN UDK- ALKA INTERGENIC REGION		UNCLASSIFIED	1039
3599	11768047 (4225, 4226)	Novel Protein sim. GBank gil2506697 sp P46490 YFCA_HAEIN - HYPOTHETICAL PROTEIN HI0198		UNCLASSIFIED	1022
3600	10372158 (13799, 13800)	Novel Protein sim. GBank gil2506712 sp P37350 YGDH_ECOLI - HYPOTHETICAL 51.0 KD PROTEIN IN BARA- SDAC INTERGENIC REGION		UNCLASSIFIED	1044
3601	20429935 (17113, 17114)	Novel Protein sim. GBank gil2507089 sp P31554 OSTA_ECOLI - ORGANIC SOLVENT TOLERANCE PROTEIN PRECURSOR		UNCLASSIFIED	1010
3602	80499554 (22967, 22968)	Novel Protein sim. GBank gil2507128 sp Q03336 SM30_RAT - SENESCENCE MARKER PROTEIN-30 (SMP-30) (REGUCALCIN) (RC)		UNCLASSIFIED	1012

3603	20177101 (17499, 17500)	Novel Protein sim. GBank gil2507435 sp P07813 SYL_ECOLI - LEUCYL- TRNA SYNTHETASE (LEUCINE--TRNA LIGASE) (LEURS)	UNCLASSIFIED	1010
3604	80027060 (15023, 15024)	Novel Protein sim. GBank gil2507450 sp P43531 YNFM_ECOLI - HYPOTHETICAL 45.3 KD PROTEIN IN MLC-ASR INTERGENIC REGION	UNCLASSIFIED	1003, 1006, 1009, 1023, 1024, 1054
3605	28455892 (17853, 17854)	Novel Protein sim. GBank gil2566534 (AF026066) - sulfite reductase [<i>Pseudomonas aeruginosa</i>]	UNCLASSIFIED	1003
3606	86380010 (4081, 4082)	Novel Protein sim. GBank gil2576345 (AC002400) - Acyl carrier protein, Mitochondrial (ACP) (5'partial) [<i>Homo sapiens</i>]	UNCLASSIFIED	1053
3607	17892336 (5607, 5608)	Novel Protein sim. GBank gil2578384 emb CAA15469] - (AL008609) glycine cleavage system h protein [<i>Mycobacterium leprae</i>]	UNCLASSIFIED	1039
3608	11419478 (20695, 20696)	Novel Protein sim. GBank gil2582195 (AF017444) - NADP-dependent malic enzyme; TME [<i>Sinorhizobium meliloti</i>]	UNCLASSIFIED	1017
3609	14401728 (6331, 6332)	Novel Protein sim. GBank gil2584886 (AF020706) - methylase HpyI [<i>Helicobacter pylori</i>]	UNCLASSIFIED	1053
3610	80059383 (1257, 1258)	Novel Protein sim. GBank gil2612814 emb CAA15531] - (AL008883) hypothetical protein Rv2869c [<i>Mycobacterium tuberculosis</i>]	UNCLASSIFIED	1012, 1024
3611	25259035 (6957, 6958)	Novel Protein sim. GBank gil2612814 emb CAA15531] - (AL008883) hypothetical protein Rv2869c [<i>Mycobacterium tuberculosis</i>]	UNCLASSIFIED	1026
3612	65488385 (5181, 5182)	Novel Protein sim. GBank gil2621621 (AE000837) - cationic amino acid transporter related protein [<i>Methanobacterium thermoautotrophicum</i>]	UNCLASSIFIED	1023

3613	65688850 (22599, 22600)	Novel Protein sim. GBank gi 2622301 (AE000887) - transcriptional regulator [Methanobacterium thermoautotrophicum]	UNCLASSIFIED	1041
3614	77520851 (12163, 12164)	Novel Protein sim. GBank gi 2622544 (AE000905) - branched-chain amino-acid aminotransferase [Methanobacterium thermoautotrophicum]	UNCLASSIFIED	1049
3615	66490065 (10173, 10174)	Novel Protein sim. GBank gi 2622939 (AE000934) - phytoene dehydrogenase [Methanobacterium thermoautotrophicum]	UNCLASSIFIED	1029
3616	20289991 (433, 434)	Novel Protein sim. GBank gi 2624270 (emb CAA15544) - (AL008967) ftsK [Mycobacterium tuberculosis]	UNCLASSIFIED	1034
3617	79564053 (4517, 4518)	Novel Protein sim. GBank gi 2626833 (dbj BAA23410) - (D86947) chemotactic transducer [Pseudomonas aeruginosa]	UNCLASSIFIED	1017
3618	85518302 (7081, 7082)	Novel Protein sim. GBank gi 2632048 (emb CAA05607) - (AJ002571) YkoJ [Bacillus subtilis]	UNCLASSIFIED	1049
3619	20446754 (2043, 2044)	Novel Protein sim. GBank gi 2632362 (emb CAB11871) - (Z99104) similar to hypothetical proteins [Bacillus subtilis]	UNCLASSIFIED	1024
3620	20297916 (16528, 16530)	Novel Protein sim. GBank gi 2632999 (emb CAB12505) - (Z99107) similar to hypothetical proteins [Bacillus subtilis]	UNCLASSIFIED	1034
3621	20456427 (12383, 12384)	Novel Protein sim. GBank gi 2633557 (emb CAB13060) - (Z99110) yjF [Bacillus subtilis]	UNCLASSIFIED	1010
3622	78378110 (14539, 14540)	Novel Protein sim. GBank gi 2633808 (emb CAB13310) - (Z99111) similar to hypothetical proteins [Bacillus subtilis]	UNCLASSIFIED	1026
3623	37801362 (3029, 3030)	Novel Protein sim. GBank gi 2633966 (emb CAB13467) - (Z99112) chromosome segregation SMC protein homolog [Bacillus subtilis]	UNCLASSIFIED	1012

3624	20177438 (3155, 3156)	Novel Protein sim. GBank gjl2634113[emb]CAB13613] - (Z99113) multidrug resistance protein [Bacillus subtilis]		UNCLASSIFIED	1010
3625	27968545 (1929, 1930)	Novel Protein sim. GBank gjl2635246[emb]CAB14741] - (Z99118) similar to sodium/proton-dependent alanine carrier protein [Bacillus subtilis]		UNCLASSIFIED	1006
3626	91219035 (8257, 8258)	Novel Protein sim. GBank gjl2635598[emb]CAB15092] - (Z99119) similar to cysteine dioxygenase [Bacillus subtilis]		UNCLASSIFIED	1044
3627	23302606 (1417, 1418)	Novel Protein sim. GBank gjl2635736[emb]CAB15229] - (Z99120) yunF [Bacillus subtilis]		UNCLASSIFIED	1023
3628	79485383 (3293, 3294)	Novel Protein sim. GBank gjl2635857[emb]CAB15349] - (Z99121) similar to sulfite reductase [Bacillus subtilis]		UNCLASSIFIED	1022
3629	55005423 (5975, 5976)	Novel Protein sim. GBank gjl2642222 (AF030885) - telomere-associated recQ-like helicase [Ustilago maydis]		UNCLASSIFIED	1019
3630	79477093 (16119, 16120)	Novel Protein sim. GBank gjl2642222 (AF030885) - telomere-associated recQ-like helicase [Ustilago maydis]		UNCLASSIFIED	1038
3631	25149365 (10293, 10294)	Novel Protein sim. GBank gjl2645861 (AF034211) - transposase OrfB [Desulfovibrio vulgaris]		UNCLASSIFIED	1003
3632	35900228 (6663, 6664)	Novel Protein sim. GBank gjl2648185 (AE000943) - carboxylesterase (est-3) [Archaeoglobus fulgidus]		UNCLASSIFIED	1053
3633	78728870 (17517, 17518)	Novel Protein sim. GBank gjl2648509 (AE000963) - conserved hypothetical protein [Archaeoglobus fulgidus]		UNCLASSIFIED	1026
3634	20721136 (5837, 5838)	Novel Protein sim. GBank gjl2649054 (AE000998) - long-chain-fatty-acid-CoA ligase (fadD-6) [Archaeoglobus fulgidus]		UNCLASSIFIED	1006

3635	13501107 (4547, 4548)	Novel Protein sim. GBank gij2649711 (AE001042) - ribose ABC transporter, permease protein (rbsC-1) [Archaeoglobus fulgidus]		UNCLASSIFIED	1027
3636	52560096 (445, 446)	Novel Protein sim. GBank gij2650614 (AE001104) - conserved hypothetical protein [Archaeoglobus fulgidus]		UNCLASSIFIED	1003, 1034
3637	79581304 (14881, 14882)	Novel Protein sim. GBank gij2655293 (AF032975) - germin-like protein 5 [Oryza sativa]		UNCLASSIFIED	1024
3638	88095003 (8443, 8444)	Novel Protein sim. GBank gij2661691[emb]CAA15795] - (AL009204) putative protease [Streptomyces coelicolor]		UNCLASSIFIED	1010, 1022
3639	80072425 (1363, 1364)	Novel Protein sim. GBank gij2661697[emb]CAA15801] - (AL009204) hypothetical protein SC9B10.11 [Streptomyces coelicolor]		UNCLASSIFIED	1003, 1006, 1008, 1022, 1023, 1024, 1038
3640	78893730 (15593, 15594)	Novel Protein sim. GBank gij2662167[dbj]BAA23715] - (AB007903) KIAA0443 [Homo sapiens]		UNCLASSIFIED	1000, 1003, 1008, 1017, 1026
3641	9945112 (4375, 4376)	Novel Protein sim. GBank gij2662366[dbj]BAA23667] - (D86332) membrane type-2 matrix metalloproteinase [Mus musculus]		UNCLASSIFIED	1044
3642	94651275 (19429, 19430)	Novel Protein sim. GBank gij266541[sp]P30746[MOAB_ECOLI - MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN B		UNCLASSIFIED	1027
3643	79831223 (20635, 20636)	Novel Protein sim. GBank gij267417[sp]P29955[XANA_XANCP - PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM) / PHOSPHOMANNOMUTASE (PMM)		UNCLASSIFIED	1023
3644	19642417 (5411, 5412)	Novel Protein sim. GBank gij2686013 (AE001124) - hemolysin III (ypIQ) [Borrelia burgdorferi]		UNCLASSIFIED	1010

3645	85818145 (2245, 2246)	Novel Protein sim. GBank gj2688536 (AE001162) - conserved hypothetical protein [Borrelia burgdorferi]		UNCLASSIFIED	1019
3646	47657227 (16139, 16140)	Novel Protein sim. GBank gj2695836[emb]CAA15906] - (AL021006) hypothetical protein Rv1250 [Mycobacterium tuberculosis]		UNCLASSIFIED	1026, 1029
3647	29647423 (13861, 13862)	Novel Protein sim. GBank gj2695957[emb]CAA15850] - (AL010186) hypothetical protein Rv1173 [Mycobacterium tuberculosis]		UNCLASSIFIED	1024
3648	10142304 (1641, 1642)	Novel Protein sim. GBank gj2695962[emb]CAA15855] - (AL010186) hypothetical protein Rv1178 [Mycobacterium tuberculosis]		UNCLASSIFIED	1054
3649	77822309 (2471, 2472)	Novel Protein sim. GBank gj2708660 (AF037440) - putative 30.6 kDa protein [Edwardsiella ictaluri]		UNCLASSIFIED	1022
3650	32152988 (16787, 16788)	Novel Protein sim. GBank gj2708660 (AF037440) - putative 30.6 kDa protein [Edwardsiella ictaluri]		UNCLASSIFIED	1023
3651	25286105 (2863, 2864)	Novel Protein sim. GBank gj2708666 (AF037441) - putative 54.5 kDa protein [Edwardsiella ictaluri]		UNCLASSIFIED	1054
3652	20288333 (4147, 4148)	Novel Protein sim. GBank gj2708666 (AF037441) - putative 54.5 kDa protein [Edwardsiella ictaluri]		UNCLASSIFIED	1034
3653	34868408 (18407, 18408)	Novel Protein sim. GBank gj2708741 (AC003952) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	1034
3654	30258500 (22937, 22938)	Novel Protein sim. GBank gj2731767 (AF016099) - endonuclease/reverse transcriptase [Mus musculus]		UNCLASSIFIED	1044
3655	28387395 (21361, 21362)	Novel Protein sim. GBank gj2736155 (AF022082) - sulfolipid biosynthesis protein [Arabidopsis thaliana]		UNCLASSIFIED	1017

3656	80025234 (12167, 12168)	Novel Protein sim. GBank gij2760909 (AF036925) - family 10 xylanase [Caldicellulosiptor sp. R169B.1]	UNCLASSIFIED	1003, 1004
3657	27977410 (875, 876)	Novel Protein sim. GBank gij2764873[emb]CAA665571 - (X97918) gene 18.1 [Bacteriophage SPP1]	UNCLASSIFIED	1006
3658	10077458 (2323, 2324)	Novel Protein sim. GBank gij2764873[emb]CAA665571 - (X97918) gene 18.1 [Bacteriophage SPP1]	UNCLASSIFIED	1038
3659	27977572 (20039, 20040)	Novel Protein sim. GBank gij2764873[emb]CAA665571 - (X97918) gene 18.1 [Bacteriophage SPP1]	UNCLASSIFIED	1006
3660	47652014 (18947, 18948)	Novel Protein sim. GBank gij2765081[emb]CAA715891 - (Y10557) g5bf [Arabidopsis thaliana]	UNCLASSIFIED	1029
3661	11130354 (21937, 21938)	Novel Protein sim. GBank gij2765453[emb]CAA755391 - (Y15252) nitrate extrusion protein [Pseudomonas aeruginosa]	UNCLASSIFIED	1006
3662	20434582 (14167, 14168)	Novel Protein sim. GBank gij2772914 (AF029249) - precollagen D [Mytilus edulis]	UNCLASSIFIED	1022
3663	78379687 (12757, 12758)	Novel Protein sim. GBank gij2780178[emb]CAA380471 - (X54111) putative enol-pyruvyltransferase [Treponema pallidum]	UNCLASSIFIED	1003, 1026
3664	20437191 (8043, 8044)	Novel Protein sim. GBank gij2791398[emb]CAA159941 - (AL021184) hypothetical protein Rv1464 [Mycobacterium tuberculosis]	UNCLASSIFIED	1010
3665	79870655 (13925, 13926)	Novel Protein sim. GBank gij2791423[emb]CAA16017.11 - (AL021185) bcp [Mycobacterium tuberculosis]	UNCLASSIFIED	1012
3666	57629037 (16449, 16450)	Novel Protein sim. GBank gij2791423[emb]CAA16017.11 - (AL021185) bcp [Mycobacterium tuberculosis]	UNCLASSIFIED	1012
3667	78373648 (11053, 11054)	Novel Protein sim. GBank gij2791495[emb]CAA160321 - (AL021246) hypothetical protein Rv2455c [Mycobacterium tuberculosis]	UNCLASSIFIED	1008, 1026

3668	78526486 (19473, 19474)	Novel Protein sim. GBank gil2791516[emb]CAA16053] - (AL021246) hypothetical protein Rv2476c [Mycobacterium tuberculosis]		UNCLASSIFIED	1001, 1008, 1026, 1029
3669	80060189 (12139, 12140)	Novel Protein sim. GBank gil2791626[emb]CAA16113.1] - (AL021287) fixB [Mycobacterium tuberculosis]		UNCLASSIFIED	1022, 1024
3670	38434691 (12423, 12424)	Novel Protein sim. GBank gil2801417 (AF007777) - KpsD [Escherichia coli]		UNCLASSIFIED	1008
3671	78474846 (393, 394)	Novel Protein sim. GBank gil280630[pir]A60095 - larval glue protein Lgp-1 precursor - fruit fly (Drosophila virilis)		UNCLASSIFIED	1026
3672	78182342 (9261, 9262)	Novel Protein sim. GBank gil2811055[sp]O07395[YS02_MYCAV - HYPOTHETICAL 36.1 KD PROTEIN MAV335]		UNCLASSIFIED	1029, 1053
3673	10069458 (6365, 6366)	Novel Protein sim. GBank gil2815577 (AF012101) - VceA [Vibrio cholerae]		UNCLASSIFIED	1012
3674	27923447 (3403, 3404)	Novel Protein sim. GBank gil2822117[sp]P16917[RHSB_ECOLI - RHSB PROTEIN PRECURSOR]		UNCLASSIFIED	1004, 1010
3675	78700877 (12453, 12454)	Novel Protein sim. GBank gil2826876[emb]CAA76170] - (Y16311) GidB-like protein [Streptomyces coelicolor]		UNCLASSIFIED	1008, 1016, 1026
3676	20606886 (20373, 20374)	Novel Protein sim. GBank gil2827587[emb]CAA16842] - (AL021646) hypothetical protein Rv3177 [Mycobacterium tuberculosis]		UNCLASSIFIED	1004
3677	80500698 (2239, 2240)	Novel Protein sim. GBank gil2827589[emb]CAA16644] - (AL021646) hypothetical protein Rv3179 [Mycobacterium tuberculosis]		UNCLASSIFIED	1012, 1017, 1026
3678	87451432 (21977, 21978)	Novel Protein sim. GBank gil2829433[sp]P52279[PIP_XANCI - PROLINE IMINOPEPTIDASE (PROLYL AMINOPEPTIDASE)]		UNCLASSIFIED	1008, 1025

3679	100822229 (4451, 4452)	Novel Protein sim. GBank gil2829512 sp P71571 YT36_MYCTU - HYPOTHETICAL PROTEIN CY10D7.36C		UNCLASSIFIED	1044
3680	66256564 (1917, 1918)	Novel Protein sim. GBank gil2829802 sp P94408 YCLF_BACSU - HYPOTHETICAL 53.3 KD PROTEIN IN SFP- GERKA INTERGENIC REGION		UNCLASSIFIED	1006, 1010, 1012, 1058
3681	78377705 (11489, 11490)	Novel Protein sim. GBank gil2829815 sp P95095 CSTA_MYCTU - CARBON STARVATION PROTEIN A HOMOLOG		UNCLASSIFIED	1026, 1029, 1053
3682	20477336 (20621, 20622)	Novel Protein sim. GBank gil2829827 sp P96194 YIBL_AZOV1 - HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN IBPB-LEUC INTERGENIC REGION		UNCLASSIFIED	1024
3683	29444840 (9481, 9482)	Novel Protein sim. GBank gil2829910 (AC002291) - Unknown protein, contains regulator of chromosome condensation motifs [Arabidopsis thaliana]		UNCLASSIFIED	1026
3684	20159983 (5491, 5492)	Novel Protein sim. GBank gil283045 pir S28264 - hydroxyproline-rich glycoprotein - maize		UNCLASSIFIED	1010
3685	10315215 (17821, 17822)	Novel Protein sim. GBank gil283045 pir S28264 - hydroxyproline-rich glycoprotein - maize		UNCLASSIFIED	1038
3686	38920403 (707, 708)	Novel Protein sim. GBank gil2832644 emb CAA16719 - (AL021710) teosinte branched1 - like protein [Arabidopsis thaliana]		UNCLASSIFIED	1008
3687	47654615 (9877, 9878)	Novel Protein sim. GBank gil2832685 emb CAA16785.1 - (AL021712) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	1029
3688	78519937 (15775, 15776)	Novel Protein sim. GBank gil2833210 sp Q07729 YD3C_YEAST - HYPOTHETICAL 55.2 KD PROTEIN YDL238C		UNCLASSIFIED	1009

3689	65709078 (12223, 12224)	Novel Protein sim. GBank gij2833435[sp]Q50049 YNTB_MYCLE - HYPOTHETICAL 41.1 KD PROTEIN (NTRB)		UNCLASSIFIED	1023
3690	3580786 (5575, 5576)	Novel Protein sim. GBank gij2833647 (AF027972) - flagelliform silk protein [Nephila clavipes]		UNCLASSIFIED	1012
3691	78761616 (18679, 18680)	Novel Protein sim. GBank gij285118 pir S27880 - Nasopressin receptor - rat		UNCLASSIFIED	1017
3692	94686125 (18119, 18120)	Novel Protein sim. GBank gij2851412[sp]Q10817 YX27_MYCTU - HYPOTHETICAL 40.1 KD PROTEIN CY274.27C		UNCLASSIFIED	1001, 1054
3693	80245905 (1511, 1512)	Novel Protein sim. GBank gij2851427[sp]P32427 PCAB_PSEPU - 3- CARBOXY-CIS,CIS-MUCONATE CYCLOISOMERASE (3-CARBOXYMUCONATE LACTONIZING ENZYME) (CMLE)		UNCLASSIFIED	1004, 1006, 1009, 1010, 1022, 1023, 1024, 1034, 1039, 1049
3694	10200283 (10187, 10188)	Novel Protein sim. GBank gij2851439[sp]P27851 UBIE_ECOLI - UBIQUINONE/MENAQUINONE BIOSYNTHESIS METHYLTRANSFERASE UBIE		UNCLASSIFIED	1039
3695	39362438 (7231, 7232)	Novel Protein sim. GBank gij2851600[sp]P33999 YJJG_ECOLI - HYPOTHETICAL 25.3 KD PROTEIN IN RIMI- PRFC INTERGENIC REGION		UNCLASSIFIED	1010, 1025
3696	27783323 (20295, 20296)	Novel Protein sim. GBank gij2851600[sp]P33999 YJJG_ECOLI - HYPOTHETICAL 25.3 KD PROTEIN IN RIMI- PRFC INTERGENIC REGION		UNCLASSIFIED	1001, 1034
3697	11819032 (13749, 13750)	Novel Protein sim. GBank gij2853098 emb CAA16914 - (AL021767) vacuolar protein sorting [Schizosaccharomyces pombe]		UNCLASSIFIED	1031

3698	20708475 (12553, 12564)	Novel Protein sim. GBank gij285355 pir [B43936 - ORF 3' of ctsA - Bacillus sp. (fragment)]	UNCLASSIFIED	1022
3699	80242645 (6011, 6012)	Novel Protein sim. GBank gij2854153 (AF045640) - No definition line found [Caenorhabditis elegans]	UNCLASSIFIED	1008, 1022
3700	13084358 (20685, 20686)	Novel Protein sim. GBank gij2854158 gb AAC02577.1] - (AF045641) No definition line found [Caenorhabditis elegans]	UNCLASSIFIED	1006, 1024
3701	36999028 (8533, 8534)	Novel Protein sim. GBank gij2865134 dbj BAA24794] - (AB001577) low specificity L-threonine aldolase [Pseudomonas sp.]	UNCLASSIFIED	1001
3702	29353027 (7629, 7630)	Novel Protein sim. GBank gij2887409 dbj BAA24847] - (AB007877)	UNCLASSIFIED	1008
3703	30258387 (16089, 16090)	Novel Protein sim. GBank KIAA0417 [Homo sapiens]	UNCLASSIFIED	1026
3704	13084619 (14043, 14044)	Novel Protein sim. GBank gij2887409 dbj BAA24847] - (AB007877)	UNCLASSIFIED	1022
3705	79116888 (20753, 20754)	Novel Protein sim. GBank gij2894252 emb CAA17114.1] - (AL021841) hypothetical protein Rv3342 [Mycobacterium tuberculosis]	UNCLASSIFIED	1013
3706	65486539 (21115, 21116)	Novel Protein sim. GBank gij2896704 emb CAA17183.1] - (AL021897) PE_PGRS [Mycobacterium tuberculosis]	UNCLASSIFIED	1010
3707	78461255 (12331, 12332)	Novel Protein sim. GBank gij2896706 emb CAA17185.1] - (AL021897) hypothetical protein Rv1069c [Mycobacterium tuberculosis]	UNCLASSIFIED	1026
3708	20594204 (16429, 16430)	Novel Protein sim. GBank gij2896706 emb CAA17185.1] - (AL021897) hypothetical protein Rv1069c [Mycobacterium tuberculosis]	UNCLASSIFIED	1058

3709	79181031 (1031, 1032)	Novel Protein sim. GBank gi 2896708 emb CAA17187.1 - (AL021897) echA9 [Mycobacterium tuberculosis]		UNCLASSIFIED	1027
3710	27341956 (9273, 9274)	Novel Protein sim. GBank gi 2896715 emb CAA17194.1 - (AL021897) pra [Mycobacterium tuberculosis]		UNCLASSIFIED	1039, 1044
3711	78468405 (17755, 17756)	Novel Protein sim. GBank gi 2896721 emb CAA17200.1 - (AL021897) hypothetical protein Rv1084 [Mycobacterium tuberculosis]		UNCLASSIFIED	1026
3712	20457834 (16355, 16356)	Novel Protein sim. GBank gi 2909464 emb CAA17350 - (AL021930) fadD27 [Mycobacterium tuberculosis]		UNCLASSIFIED	1010
3713	13084995 (753, 754)	Novel Protein sim. GBank gi 2909501 emb CAA17386 - (AL021931) hypothetical protein Rv0380c [Mycobacterium tuberculosis]		UNCLASSIFIED	1027
3714	20632801 (4917, 4918)	Novel Protein sim. GBank gi 2909643 emb CAA17455 - (AL021942) hypothetical protein Rv0584 [Mycobacterium tuberculosis]		UNCLASSIFIED	1004
3715	28836453 (7711, 7712)	Novel Protein sim. GBank gi 2911073 emb CAA17535.1 - (AL021960) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	1017
3716	79863543 (2821, 2822)	Novel Protein sim. GBank gi 2920625 (AF044499) - vgrE protein [Escherichia coli]		UNCLASSIFIED	1003, 1054
3717	14973796 (18303, 18304)	Novel Protein sim. GBank gi 2920625 (AF044499) - vgrE protein [Escherichia coli]		UNCLASSIFIED	1027
3718	10331526 (17165, 17166)	Novel Protein sim. GBank gi 2921304 (AF033496) - herbicide safener binding protein [Zea mays]		UNCLASSIFIED	1023
3719	94991905 (3385, 3386)	Novel Protein sim. GBank gi 2924463 emb CAA17703 - (AL022021) hypothetical protein Rv1781c [Mycobacterium tuberculosis]		UNCLASSIFIED	1001, 1010, 1027, 1031, 1034, 1039

3720	78677596 (9835, 9836)	Novel Protein sim. GBank gi 2924463 emb CAA17703 - (AL022021) hypothetical protein Rv1781c [Mycobacterium tuberculosis]		UNCLASSIFIED	1008
3721	20292492 (15637, 15638)	Novel Protein sim. GBank gi 2935296 (AF037272) - WAP four-disulfide core domain protein [Rattus norvegicus]		UNCLASSIFIED	1022
3722	9896796 (2913, 2914)	Novel Protein sim. GBank gi 2947269 (AF049243) - symbiosis island integrase [Mesorhizobium loti]		UNCLASSIFIED	1017
3723	79233571 (21505, 21506)	Novel Protein sim. GBank gi 2950437 emb CAA17840 - (AL022073) hypothetical protein Rv1967 [Mycobacterium tuberculosis]		UNCLASSIFIED	1001
3724	79572946 (15021, 15022)	Novel Protein sim. GBank gi 2950440 emb CAA17843 - (AL022073) [prM [Mycobacterium tuberculosis]		UNCLASSIFIED	1016, 1044
3725	42941696 (868, 870)	Novel Protein sim. GBank gi 295597 (L16548) - cell division cycle protein [Saccharomyces cerevisiae]		UNCLASSIFIED	1050
3726	88094595 (9437, 9438)	Novel Protein sim. GBank gi 2960082 emb CAA17980.1 - (AL022121) hypothetical protein Rv3658c [Mycobacterium tuberculosis]		UNCLASSIFIED	1004, 1026, 1031
3727	25241750 (17409, 17410)	Novel Protein sim. GBank gi 2960083 emb CAA17981.1 - (AL022121) trbB [Mycobacterium tuberculosis]		UNCLASSIFIED	1044
3728	9875524 (8611, 8612)	Novel Protein sim. GBank gi 2960154 emb CAA18052.1 - (AL022121) hypothetical protein Rv3730c [Mycobacterium tuberculosis]		UNCLASSIFIED	1044
3729	79835199 (4161, 4162)	Novel Protein sim. GBank gi 2960161 emb CAA18059.1 - (AL022121) hypothetical protein Rv3737 [Mycobacterium tuberculosis]		UNCLASSIFIED	1009, 1023, 1027

3730	20434462 (16463, 16464)	Novel Protein sim. GBank gil2960173 emb CAA1807.1.1 - (AL022121) hypothetical protein Rv3749c [Mycobacterium tuberculosis]		UNCLASSIFIED	1022
3731	94322180 (21317, 21318)	Novel Protein sim. GBank gil296594 emb CAA48592 - (X68600) pZE40 [Hordeum vulgare]		UNCLASSIFIED	1044
3732	78925817 (8199, 8200)	Novel Protein sim. GBank gil2970646 (AF051945) - Xin [Mus musculus]		UNCLASSIFIED	1009, 1039
3733	11807057 (20031, 20032)	Novel Protein sim. GBank gil2981042 (AF051690) - hydroxamate-type ferrisiderophore receptor [Pseudomonas aeruginosa]		UNCLASSIFIED	1017
3734	99388795 (10205, 10206)	Novel Protein sim. GBank gil2981221 (AF053091) - eyelid [Drosophila melanogaster]		UNCLASSIFIED	1003, 1004, 1010, 1012, 1017, 1044, 1054
3735	20747754 (14705, 14706)	Novel Protein sim. GBank gil2981221 (AF053091) - eyelid [Drosophila melanogaster]		UNCLASSIFIED	1022
3736	65891394 (593, 594)	Novel Protein sim. GBank gil2981631 dbj BAA25253.1 - (AB012223) ORF2 [Canis familiaris]		UNCLASSIFIED	1054
3737	86466230 (3331, 3332)	Novel Protein sim. GBank gil2981631 dbj BAA25253.1 - (AB012223) ORF2 [Canis familiaris]		UNCLASSIFIED	1029
3738	32184749 (8801, 8802)	Novel Protein sim. GBank gil2981631 dbj BAA25253.1 - (AB012223) ORF2 [Canis familiaris]		UNCLASSIFIED	1029
3739	70079161 (11033, 11034)	Novel Protein sim. GBank gil2981631 dbj BAA25253.1 - (AB012223) ORF2 [Canis familiaris]		UNCLASSIFIED	1042
3740	90936390 (15107, 15108)	Novel Protein sim. GBank gil2981631 dbj BAA25253.1 - (AB012223) ORF2 [Canis familiaris]		UNCLASSIFIED	1020
3741	94132221 (16473, 16474)	Novel Protein sim. GBank gil2981631 dbj BAA25253.1 - (AB012223) ORF2 [Canis familiaris]		UNCLASSIFIED	1003

1054	Urinary System/Kidney	cancer, trauma, regeneration (in vitro and in vivo), viral/bacterial/parasitic infections	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
1055	Urinary System/Kidney/Kidney Cortex	cancer, trauma, regeneration (in vitro and in vivo), viral/bacterial/parasitic infections	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
1056	Urinary System/Kidney/Kidney Cortex/Nephrons/Proximal Convoluted Tubule	cancer, trauma, regeneration (in vitro and in vivo), viral/bacterial/parasitic infections	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
1057	Urinary System/Urinary Bladder	cancer, trauma, regeneration (in vitro and in vivo), viral/bacterial/parasitic infections	cystitis, incontinence
1058	Whole Organism	cancer, trauma, tissue regeneration (in vitro and in vivo), viral/bacterial/parasitic infections, immunological disease, respiratory disease, gastro-intestinal diseases, reproductive health, neurological and neurodegenerative diseases, bone marrow transplantation, metabolic and endocrine diseases, allergy and inflammation, nephrological disorders, cardiovascular diseases, muscle, bone, joint and skeletal disorders, hematopoietic disorders, urinary system disorders	

3742	95292743 (17239, 17240)	Novel Protein sim. GBank gj 2982986 (AE000682) - putative protein [Aquifex aeolicus]		UNCLASSIFIED	1001, 1003, 1004, 1006, 1010, 1017, 1024, 1034, 1038, 1044
3743	86484818 (10959, 10960)	Novel Protein sim. GBank gj 2982990 (AE000682) - hypothetical protein [Aquifex aeolicus]		UNCLASSIFIED	1003, 1004, 1008, 1009, 1012, 1022, 1027, 1029, 1031, 1039
3744	79854963 (12121, 12122)	Novel Protein sim. GBank gj 2983155 (AE000693) - phosphoglucosyltransferase/phosphomannomutase [Aquifex aeolicus]		UNCLASSIFIED	1022, 1023, 1026
3745	78738893 (1655, 1656)	Novel Protein sim. GBank gj 2983161 (AE000693) - hypothetical protein [Aquifex aeolicus]		UNCLASSIFIED	1016, 1029, 1044
3746	7958708 (19067, 19068)	Novel Protein sim. GBank gj 2983239 (AE000699) - penicillin binding protein 1A [Aquifex aeolicus]		UNCLASSIFIED	1003
3747	86672776 (17887, 17888)	Novel Protein sim. GBank gj 2983296 (AE000703) - N-methylhydantoinase A [Aquifex aeolicus]		UNCLASSIFIED	1048
3748	80249045 (12865, 12866)	Novel Protein sim. GBank gj 2983973 (AE000748) - hypothetical protein [Aquifex aeolicus]		UNCLASSIFIED	1022, 1034
3749	35933537 (20457, 20458)	Novel Protein sim. GBank gj 2984142 (AE000760) - preprotein translocase SecA subunit [Aquifex aeolicus]		UNCLASSIFIED	1053
3750	18568845 (9159, 9160)	Novel Protein sim. GBank gj 2984162 (AE000761) - hypothetical protein [Aquifex aeolicus]		UNCLASSIFIED	1001
3751	19847636 (891, 892)	Novel Protein sim. GBank gj 2984771 (AF054622) - PhpA [Pseudomonas aeruginosa]		UNCLASSIFIED	1034

3752	82124653 (8679, 8680)	Novel Protein sim. GBank gi 298642 bbs 127516 - (S57132) type XVI collagen alpha 1 chain, alpha 1 (XVI) [human, placenta, Peptide Partial, 1186 aa] [-Homo sapiens]		UNCLASSIFIED	1008, 1010, 1016, 1044, 1054
3753	80255581 (6159, 6160)	Novel Protein sim. GBank gi 2995273 emb CAA06222] - (AJ004922) aminopeptidase [Lycopersicon esculentum]		UNCLASSIFIED	1006
3754	11398597 (1939, 1940)	Novel Protein sim. GBank gi 2995344 emb CAA18298] - (AL022244) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	1006
3755	82368284 (3589, 3590)	Novel Protein sim. GBank gi 2995352 emb CAA04606.1] - (AJ001206) pep1 [Streptomyces coelicolor]		UNCLASSIFIED	1001, 1006, 1008, 1010, 1022, 1023, 1024, 1030, 1038
3756	79831387 (19009, 19010)	Novel Protein sim. GBank gi 2996039 (AF054525) - hypothetical protein [Synecococcus PCC7002]		UNCLASSIFIED	1023, 1039
3757	80059952 (21999, 22000)	Novel Protein sim. GBank gi 29966650 (AC004493) - KIAA0324 [Homo sapiens]		UNCLASSIFIED	1024
3758	85538523 (12233, 12234)	Novel Protein sim. GBank gi 3002527 (AF010144) - neuronal thread protein AD7c-NTP [Homo sapiens]		UNCLASSIFIED	1054
3759	21660822 (3583, 3584)	Novel Protein sim. GBank gi 3006178 emb CAA18398.1] - (AL022304) putative mrna transport regulator [Schizosaccharomyces pombe]		UNCLASSIFIED	1024
3760	10920989 (21697, 21698)	Novel Protein sim. GBank gi 3023676 sp P56287 E2BE_SCHPO - PROBABLE TRANSLATION INITIATION FACTOR EIF-2B EPSILON SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR)		UNCLASSIFIED	1024
3761	78498961 (3341, 3342)	Novel Protein sim. GBank gi 3024154 sp Q92794 MOZ_HUMAN - MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN		UNCLASSIFIED	1016, 1024

3762	80209634 (5713, 5714)	Novel Protein sim. GBank gil3024675 sp P56417 SYN_HELPY - TYROSYL-TRNA SYNTHETASE (TYROSINE--TRNA LIGASE) (TYRRS)		UNCLASSIFIED	1034
3763	78477090 (19523, 19524)	Novel Protein sim. GBank gil3024715 sp O08807 TDXN_MOUSE - ANTIOXIDANT ENZYME AOE372		UNCLASSIFIED	1003
3764	3692426 (16455, 16456)	Novel Protein sim. GBank gil3024732 sp Q58432 THIC_METJA - PROBABLE THIAMIN BIOSYNTHESIS PROTEIN THIC		UNCLASSIFIED	1012
3765	78835864 (7607, 7608)	Novel Protein sim. GBank gil3025127 sp P76235 YEAH_ECOLI - HYPOTHETICAL 49.4 KD PROTEIN IN GAPA-RND INTERGENIC REGION		UNCLASSIFIED	1008
3766	25165226 (16229, 16230)	Novel Protein sim. GBank gil3025162 sp P76369 YEEY_ECOLI - HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN SBCB-HISL INTERGENIC REGION		UNCLASSIFIED	1003
3767	79912109 (14655, 14656)	Novel Protein sim. GBank gil3025170 sp P77500 YFER_ECOLI - HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN XAPA-LIG INTERGENIC REGION		UNCLASSIFIED	1023, 1038
3768	78800814 (9037, 9038)	Novel Protein sim. GBank gil3025276 sp Q02981 YP09_YEAST - HYPOTHETICAL 62.8 KD PROTEIN IN SSE1-CAR1 INTERGENIC REGION		UNCLASSIFIED	1026
3769	30258104 (12509, 12510)	Novel Protein sim. GBank gil3025282 sp P71691 YR40_MYCTU - HYPOTHETICAL 35.8 KD PROTEIN CY21B4.40		UNCLASSIFIED	1026
3770	80414655 (20159, 20160)	Novel Protein sim. GBank gil3025284 sp P77475 YQAB_ECOLI - HYPOTHETICAL 20.8 KD PROTEIN IN GSHA-CSRA INTERGENIC REGION		UNCLASSIFIED	1004, 1008, 1010, 1023, 1024, 1025, 1034

3771	25243584 (21071, 21072)	Novel Protein sim. GBank gij3033380 (AC004238) - putative coatomer epsilon subunit [Arabidopsis thaliana]	UNCLASSIFIED	1013
3772	78715968 (12027, 12028)	Novel Protein sim. GBank gij3043529[embjCAA05249] - (AJ002204) polyamine oxidase [Zea mays]	UNCLASSIFIED	1017
3773	78948406 (443, 444)	Novel Protein sim. GBank gij3043648[dbjBAA25488] - (AB011134) KIAA0562 protein [Homo sapiens]	UNCLASSIFIED	1044
3774	38869092 (10837, 10838)	Novel Protein sim. GBank gij3043714[dbjBAA25521] - (AB011167) KIAA0595 protein [Homo sapiens]	UNCLASSIFIED	1003
3775	56451138 (22257, 22258)	Novel Protein sim. GBank gij3043718[dbjBAA25523] - (AB011169) KIAA0597 protein [Homo sapiens]	UNCLASSIFIED	1003
3776	23299542 (13201, 13202)	Novel Protein sim. GBank gij3043882 (U95842) - transmembrane protein Tmp7 [Lactococcus lactis]	UNCLASSIFIED	1044
3777	78784542 (12987, 12988)	Novel Protein sim. GBank gij3044093 (AF055999) - hypothetical protein PhuW [Pseudomonas aeruginosa]	UNCLASSIFIED	1008
3778	79863572 (7205, 7206)	Novel Protein sim. GBank gij3046395[gbjAAC38320.1] - (AF026544) unknown [Ralstonia eutropha]	UNCLASSIFIED	1006, 1017
3779	20292854 (17149, 17150)	Novel Protein sim. GBank gij3068553 (U19489) - glycoprotein Ib [Canis familiaris]	UNCLASSIFIED	1034
3780	65641577 (13087, 13088)	Novel Protein sim. GBank gij3068592 (AF026465) - punc [Mus musculus]	UNCLASSIFIED	1016
3781	79570299 (14997, 14998)	Novel Protein sim. GBank gij3080400[embjCAA18720.1] - (AL022603) putative protein [Arabidopsis thaliana]	UNCLASSIFIED	1017
3782	78676758 (21281, 21282)	Novel Protein sim. GBank gij3080493[embjCAA18690] - (AL022602) hypothetical protein MLCB268.24c [Mycobacterium leprae]	UNCLASSIFIED	1008

3783	82439120 (22873, 22874)	Novel Protein sim. GBank gi 3088561 (AF059313) - myo-inositol dehydrogenase [Sinorhizobium meliloti]		UNCLASSIFIED	1001, 1006, 1012, 1022, 1023, 1024, 1026, 1034, 1044, 1058
3784	10187603 (12597, 12598)	Novel Protein sim. GBank gi 3095052 (AF010234) - ArsC [Pseudomonas aeruginosa]		UNCLASSIFIED	1003
3785	79485868 (9397, 9398)	Novel Protein sim. GBank gi 3097809 (L49465) - hypothetical metabolite transport protein [Pseudomonas fluorescens]		UNCLASSIFIED	1022
3786	9857702 (14403, 14404)	Novel Protein sim. GBank gi 3098342 (AF036166) - organic hydroperoxide resistance protein [Xanthomonas campestris]		UNCLASSIFIED	1008
3787	79192369 (20885, 20886)	Novel Protein sim. GBank gi 3098342 (AF036166) - organic hydroperoxide resistance protein [Xanthomonas campestris]		UNCLASSIFIED	1024
3788	80255457 (15565, 15566)	Novel Protein sim. GBank gi 3098418 (AF040944) - P140 [Mus musculus]		UNCLASSIFIED	1001, 1003, 1006, 1054
3789	20628071 (13583, 13584)	Novel Protein sim. GBank gi 309868 (L09108) - IS401 transposase subunit; putative [Pseudomonas cepacia]		UNCLASSIFIED	1010
3790	27832852 (11503, 11504)	Novel Protein sim. GBank gi 3122417 sp O33804 MURF_STRTO - PROBABLE UDP-N-ACETYLURAMIDYLALANYL-D-GLUTAMYL-2,6-DIAMINOPIMELATE-D-ALANYL-D-ALANYL-LIGASE (UDP-MURNAC-PENTAPEPTIDE SYNTHETASE) (D-ALANYL-D-ALANINE-ADDING ENZYME)		UNCLASSIFIED	1022
3791	79572143 (20141, 20142)	Novel Protein sim. GBank gi 3122893 sp P94985 SYFB_MYCTU - PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (PHENYLALANINE-TRNA LIGASE BETA CHAIN) (PHERS)		UNCLASSIFIED	1008, 1023, 1029, 1039

3792	11605975 (20539, 20540)	Novel Protein sim. GBank gi 3122893 sp P94985 SYFB_MYCTU - PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (PHENYLALANINE-TRNA LIGASE BETA CHAIN) (PHERS)		UNCLASSIFIED	1024
3793	85525006 (17111, 17112)	Novel Protein sim. GBank gi 3122905 sp O26687 SYM_METTH - METHIONYL-TRNA SYNTHETASE (METHIONINE-TRNA LIGASE) (METRS)		UNCLASSIFIED	1008, 1026, 1049
3794	20137096 (999, 1000)	Novel Protein sim. GBank gi 3122932 sp O32053 TGT_BACSU - QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA- GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)		UNCLASSIFIED	1024
3795	80216390 (6267, 6268)	Novel Protein sim. GBank gi 3123021 sp Q90508 VIT1_FUNHE - VITELLOGENIN 1 PRECURSOR (VTG I) (CONTAINS: LIPOVITELLIN 1 (LV1); PHOSVITIN (PV); LIPOVITELLIN 2 (LV2))		UNCLASSIFIED	1004, 1022
3796	80256665 (20775, 20776)	Novel Protein sim. GBank gi 3123021 sp Q90508 VIT1_FUNHE - VITELLOGENIN 1 PRECURSOR (VTG I) (CONTAINS: LIPOVITELLIN 1 (LV1); PHOSVITIN (PV); LIPOVITELLIN 2 (LV2))		UNCLASSIFIED	1006
3797	19521923 (10873, 10874)	Novel Protein sim. GBank gi 3123224 sp P17731 HIS8_BACSU - HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (IMIDAZOLE ACETOL- PHOSPHATE TRANSAMINASE)		UNCLASSIFIED	1034
3798	100328610 (13783, 13784)	Novel Protein sim. GBank gi 3123552 emb CAA18609 - (AL022578) dJ393P12.2 (hypothetical Proline-rich protein KIAA0269 LIKE) (Homo sapiens)		UNCLASSIFIED	1001, 1003, 1004, 1008, 1016, 1017, 1022, 1024, 1028, 1037, 1044, 1053, 1054

3799	20459464 (4789, 4790)	Novel Protein sim. GBank gij3127836[emb]CAA18902] - (AL023496) hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	1024
3800	39523493 (11359, 11360)	Novel Protein sim. GBank gij3128287 (AF010496) - hypothetical protein [Rhodobacter capsulatus]		UNCLASSIFIED	1004
3801	82116318 (14233, 14234)	Novel Protein sim. GBank gij3128302 (AF010496) - hypothetical protein [Rhodobacter capsulatus]		UNCLASSIFIED	1016, 1017
3802	79615799 (20363, 20364)	Novel Protein sim. GBank gij3128335 (AF010496) - precorin-3 methylase [Rhodobacter capsulatus]		UNCLASSIFIED	1003, 1044
3803	19884371 (20033, 20034)	Novel Protein sim. GBank gij3136020[emb]CAA19102] - (AL023591) hypothetical protein MLCB1259.27 [Mycobacterium leprae]		UNCLASSIFIED	1034
3804	17936961 (9697, 9698)	Novel Protein sim. GBank gij3136036[emb]CAA19115] - (AL023592) RanBP7/importin-beta/Cse1p superfamily protein [Schizosaccharomyces pombe]		UNCLASSIFIED	1008
3805	28462243 (6735, 6736)	Novel Protein sim. GBank gij3142291 (AC002411) - Contains similarity to adenylate cyclase gb AF012921 from Magnaporthe griseae. EST gb Z24512 comes from this gene. [Arabidopsis thaliana]		UNCLASSIFIED	1030
3806	78675175 (12547, 12548)	Novel Protein sim. GBank gij3142297 (AC002411) - Contains similarity to serine/threonine protein phosphatase gb X83099 from S. cerevisiae. [Arabidopsis thaliana]		UNCLASSIFIED	1017
3807	28992682 (14877, 14878)	Novel Protein sim. GBank gij3150479 (AF067212) - partial CDS [Caenorhabditis elegans]		UNCLASSIFIED	1044
3808	16510691 (17581, 17582)	Novel Protein sim. GBank gij3169045[emb]CAA19243] - (AL023702) uroporphyrinogen decarboxylase [Streptomyces coelicolor]		UNCLASSIFIED	1044

3809	79229835 (18565, 18566)	Novel Protein sim. GBank gi 3169045 emb CAA19243 - (AL023702) uroporphyrinogen decarboxylase [Streptomyces coelicolor]		UNCLASSIFIED	1006
3810	56499770 (8791, 8792)	Novel Protein sim. GBank gi 3170176 gb AAC18037.1 - (AF039688) antigen NY-CO-3 [Homo sapiens]		UNCLASSIFIED	1023
3811	80447820 (5239, 5240)	Novel Protein sim. GBank gi 3171904 emb CAA75869 - (Y15908) DIA-12C protein [Homo sapiens]		UNCLASSIFIED	1023, 1038, 1039
3812	13519669 (20053, 20054)	Novel Protein sim. GBank gi 3183185 sp O07631 TYP A_BACSU - GTP- BINDING PROTEIN TYP A/BIP A HOMOLOG		UNCLASSIFIED	1024
3813	79443070 (22617, 22618)	Novel Protein sim. GBank gi 3183185 sp O07631 TYP A_BACSU - GTP- BINDING PROTEIN TYP A/BIP A HOMOLOG		UNCLASSIFIED	1022
3814	25328062 (21129, 21130)	Novel Protein sim. GBank gi 3183467 sp O31727 YLME_BACSU - HYPOTHETICAL 25.7 KD PROTEIN IN SIGG- DIVIVA INTERGENIC REGION		UNCLASSIFIED	1017
3815	65902617 (9011, 9012)	Novel Protein sim. GBank gi 3192889 (AF068843) - dihydroxy-acid dehydratase [Streptomyces coelicolor]		UNCLASSIFIED	1023
3816	58213763 (5393, 5394)	Novel Protein sim. GBank gi 320748 pir S25330 - probable membrane protein YBL011w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006, 1022
3817	39371622 (17687, 17688)	Novel Protein sim. GBank gi 3218410 emb CAA19574.1 - (AL023859) SPBC19C7.06, putative prolyl-trna synthetase, len:71 6aa, similar eg. to YHR020W, YHI0_YEAST, P38708, putative p rolyl-trna synthetase yhr02, (688aa), fasta scores, opt.248 6, E():0, (55.1% identity in 682 aa overl...		UNCLASSIFIED	1024, 1034

3818	87452021 (18849, 18850)	Novel Protein sim. GBank gij3236247 (AC004684) - SCARECROW-like protein [Arabidopsis thaliana]	UNCLASSIFIED	1025
3819	85817932 (861, 862)	Novel Protein sim. GBank gij3236351 (AF033663) - PRP4 protein kinase homolog [Mus musculus]	UNCLASSIFIED	1019
3820	36991783 (22215, 22216)	Novel Protein sim. GBank gij3241969 (U79580) - CbpA [Pseudomonas aeruginosa]	UNCLASSIFIED	1016
3821	80503426 (18827, 18828)	Novel Protein sim. GBank gij3242273[emb]CAB07017] - (Z92669) hypothetical protein Rv0236c [Mycobacterium tuberculosis]	UNCLASSIFIED	1012
3822	32434178 (16725, 16726)	Novel Protein sim. GBank gij3242281[emb]CAA16669] - (AL021646) hypothetical protein Rv3202c [Mycobacterium tuberculosis]	UNCLASSIFIED	1012
3823	46665821 (1425, 1426)	Novel Protein sim. GBank gij3252868 (AF033536) - putative zinc transporter [Arabidopsis thaliana]	UNCLASSIFIED	1031, 1050, 1054
3824	79319731 (4099, 4100)	Novel Protein sim. GBank gij3253197 (AF029714) - PhaA [Pseudomonas putida]	UNCLASSIFIED	1053
3825	19860967 (3961, 3962)	Novel Protein sim. GBank gij3256606[dbj]BAA29289.1] - (AP000001) 171aa long hypothetical protein [Pyrococcus horikoshii]	UNCLASSIFIED	1001
3826	80027689 (19839, 19840)	Novel Protein sim. GBank gij3256692[dbj]BAA29375.1] - (AP000001) 380aa long hypothetical Na(+)/H(+) antiporter [Pyrococcus horikoshii]	UNCLASSIFIED	1004, 1024
3827	7958056 (18877, 18878)	Novel Protein sim. GBank gij3256835[dbj]BAA29518] - (AP000002) 393aa long hypothetical protein [Pyrococcus horikoshii]	UNCLASSIFIED	1044
3828	11088295 (15335, 15336)	Novel Protein sim. GBank gij3257161[dbj]BAA29844] - (AP000003) 464aa long hypothetical protein [Pyrococcus horikoshii]	UNCLASSIFIED	1004

3829	47652238 (1043, 1044)	Novel Protein sim. GBank gil3261660 emb CAB03752 - (Z81368) hypothetical protein Rv2420c [Mycobacterium tuberculosis]	UNCLASSIFIED	1029, 1034, 1053
3830	78891013 (6169, 6170)	Novel Protein sim. GBank gil3261661 emb CAB03753 - (Z81368) hypothetical protein Rv2421c [Mycobacterium tuberculosis]	UNCLASSIFIED	1003, 1039
3831	95005747 (2237, 2238)	Novel Protein sim. GBank gil3261740 emb CAB08320 - (Z95120) lipV [Mycobacterium tuberculosis]	UNCLASSIFIED	1034
3832	80467071 (12663, 12664)	Novel Protein sim. GBank gil3261775 emb CAB09037 - (Z95584) hypothetical protein Rv1165 [Mycobacterium tuberculosis]	UNCLASSIFIED	1012, 1039
3833	36827011 (22975, 22976)	Novel Protein sim. GBank gil3261775 emb CAB09037 - (Z95584) hypothetical protein Rv1165 [Mycobacterium tuberculosis]	UNCLASSIFIED	1054
3834	39517741 (4851, 4852)	Novel Protein sim. GBank gil3261780 emb CAB08931 - (Z95556) hypothetical protein Rv2511 [Mycobacterium tuberculosis]	UNCLASSIFIED	1004, 1006, 1010, 1024
3835	79319279 (9857, 9858)	Novel Protein sim. GBank gil3283977 (AF072816) - ABC-type transporter MRP3 [Rattus norvegicus]	UNCLASSIFIED	1006, 1017, 1034
3836	91012911 (14087, 14088)	Novel Protein sim. GBank gil3287951 sp O34617 YLON_BACSU - HYPOTHETICAL 41.6 KD PROTEIN IN FMT- SPOVM INTERGENIC REGION	UNCLASSIFIED	1010
3837	79846075 (7491, 7492)	Novel Protein sim. GBank gil3288157 emb CAA11510 - (AJ223631) hypothetical protein [Escherichia coli]	UNCLASSIFIED	1034
3838	37019662 (10921, 10922)	Novel Protein sim. GBank gil3294236 emb CAA19849 - (AL031031) putative sensory histidine kinase [Streptomyces coelicolor]	UNCLASSIFIED	1025

3839	34394203 (11421, 11422)	Novel Protein sim. GBank gil3294238[emb]CAA19851] - (AL031031) ftsK homolog [Streptomyces coelicolor]	UNCLASSIFIED	1026
3840	80248954 (3613, 3614)	Novel Protein sim. GBank gil3294242[emb]CAA19855] - (AL031031) hypothetical protein SC7C7.09 [Streptomyces coelicolor]	UNCLASSIFIED	1001, 1006, 1034
3841	79846720 (3625, 3626)	Novel Protein sim. GBank gil3297821[emb]CAA19879.1] - (AL031032) extensin-like protein [Arabidopsis thaliana]	UNCLASSIFIED	1003, 1023, 1044
3842	25140253 (22427, 22428)	Novel Protein sim. GBank gil3297821[emb]CAA19879.1] - (AL031032) extensin-like protein [Arabidopsis thaliana]	UNCLASSIFIED	1003, 1022
3843	11705900 (7683, 7684)	Novel Protein sim. GBank gil331897[pdb]1FOH[A - Chain A, Phenol Hydroxylase From Trichosporon Cutaneum]	UNCLASSIFIED	1022
3844	37798103 (5127, 5128)	Novel Protein sim. GBank gil3319337 (AF076530) - cell division protein FtsZ [Synecchococcus PCC7942]	UNCLASSIFIED	1012
3845	21656486 (3599, 3600)	Novel Protein sim. GBank gil3319741[emb]CAA19907] - (AL031035) hypothetical protein SC6A9.22c [Streptomyces coelicolor]	UNCLASSIFIED	1004, 1022
3846	78385459 (6633, 6634)	Novel Protein sim. GBank gil3319741[emb]CAA19907] - (AL031035) hypothetical protein SC6A9.22c [Streptomyces coelicolor]	UNCLASSIFIED	1023, 1026
3847	10330018 (17617, 17618)	Novel Protein sim. GBank gil3322862 (AE001232) - Tp70 protein [Treponema pallidum]	UNCLASSIFIED	1038
3848	79624944 (10457, 10458)	Novel Protein sim. GBank gil3322940 (AE001239) - histidyl-tRNA synthetase (hisS) [Treponema pallidum]	UNCLASSIFIED	1006
3849	36625389 (21381, 21382)	Novel Protein sim. GBank gil3327216[pdb]BAA31676] - (AB014601) KIAA0701 protein [Homo sapiens]	UNCLASSIFIED	1034

3850	11759414 (14311, 14312)	Novel Protein sim. GBank gij3327262[dbj BAA31695] - (AB010827) NhaP [Pseudomonas aeruginosa]		UNCLASSIFIED	1024
3851	29350796 (12751, 12752)	Novel Protein sim. GBank gij3328717 (AE001302) - Valyl tRNA Synthetase [Chlamydia trachomatis]		UNCLASSIFIED	1017, 1022
3852	78675172 (12297, 12298)	Novel Protein sim. GBank gij3329429 (AF049613) - huntingtin interacting protein HYPK [Homo sapiens]		UNCLASSIFIED	1009
3853	79749080 (8275, 8276)	Novel Protein sim. GBank gij3334173[sp O5834 ERA_MYCTU - GTP- BINDING PROTEIN ERA HOMOLOG		UNCLASSIFIED	1004, 1017, 1023
3854	78728420 (3575, 3576)	Novel Protein sim. GBank gij3334982 (AC005306) - R27216_1 [Homo sapiens]		UNCLASSIFIED	1022
3855	78778238 (7581, 7582)	Novel Protein sim. GBank gij3335366 (AC003028) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	1044
3856	6313219 (20937, 20938)	Novel Protein sim. GBank gij3341578[emb CAA13133] - (AJ231091) z29f [Vibrio cholerae]		UNCLASSIFIED	1058
3857	79847568 (12649, 12650)	Novel Protein sim. GBank gij3341640[emb CAA13164] - (AJ231122) z61f [Vibrio cholerae]		UNCLASSIFIED	1023, 1039
3858	78527927 (9345, 9346)	Novel Protein sim. GBank gij3355671[emb CAA19971] - (AL031124) branched-chain amino acid aminotransferase [Streptomyces coelicolor]		UNCLASSIFIED	1030
3859	79779458 (20763, 20764)	Novel Protein sim. GBank gij3355671[emb CAA19971] - (AL031124) branched-chain amino acid aminotransferase [Streptomyces coelicolor]		UNCLASSIFIED	1010, 1017, 1022, 1023, 1034, 1044
3860	81820351 (16747, 16748)	Novel Protein sim. GBank gij3355678[emb CAA19978] - (AL031124) putative secreted protein [Streptomyces coelicolor]		UNCLASSIFIED	1053, 1054

3861	80017304 (11831, 11932)	Novel Protein sim. GBank gi 3367755 emb CAA20080 - (AL031155) putative transcriptional regulator [Streptomyces coelicolor]		UNCLASSIFIED	1017, 1022, 1024
3862	10368042 (18103, 18104)	Novel Protein sim. GBank gi 3378352 (AF079317) - DNA helicase [Sphingomonas aromaticivorans]		UNCLASSIFIED	1001
3863	96001909 (8211, 8212)	Novel Protein sim. GBank gi 3399676 (AC005390) - R31180_1 [Homo sapiens]		UNCLASSIFIED	1004, 1010, 1034
3864	29213147 (17723, 17724)	Novel Protein sim. GBank gi 3402247 emb CAA20183 - (AL031184) oligopeptide ABC transporter ATP-binding protein [Streptomyces coelicolor]		UNCLASSIFIED	1026
3865	25254288 (19705, 19706)	Novel Protein sim. GBank gi 3402255 emb CAA20191 - (AL031184) tRNA (5 methylaminomethyl-2-thiouridylate)- methyltransferase [Streptomyces coelicolor]		UNCLASSIFIED	1008
3866	65902132 (4697, 4698)	Novel Protein sim. GBank gi 3406759 (AF079502) - CAMP factor [Streptococcus pyogenes]		UNCLASSIFIED	1023, 1044
3867	85801868 (12025, 12026)	Novel Protein sim. GBank gi 3406759 (AF079502) - CAMP factor [Streptococcus pyogenes]		UNCLASSIFIED	1038, 1040
3868	80255569 (3057, 3058)	Novel Protein sim. GBank gi 3411177 (AF076240) - MocC [Rhizobium leguminosarum bv. viciae]		UNCLASSIFIED	1006, 1026
3869	78271019 (5289, 5290)	Novel Protein sim. GBank gi 3413391 emb CAA20252 - (AL031231) hypothetical protein SC3C3.03c [Streptomyces coelicolor]		UNCLASSIFIED	1029
3870	33205346 (1025, 1026)	Novel Protein sim. GBank gi 3413411 emb CAA20272 - (AL031231) guanosine pentaphosphate synthetase/ polyribonucleotide nucleotidyltransferase [Streptomyces coelicolor]		UNCLASSIFIED	1026

3871	80494518 (18289, 18290)	Novel Protein sim. GBank gi 3413828 emb CAA20298 - (AL031260) hypothetical protein SC9A10.09 [Streptomyces coelicolor]		UNCLASSIFIED	1001, 1003, 1012, 1024
3872	56152202 (22843, 22844)	Novel Protein sim. GBank gi 3420233 (AF058763) - uroporphyrinogen decarboxylase [Zea mays]		UNCLASSIFIED	1008
3873	91215789 (9645, 9646)	Novel Protein sim. GBank gi 3420605 gb AAC31904.1 - (AF075709) putative sulfonate binding protein precursor [Pseudomonas putida]		UNCLASSIFIED	1016
3874	24135051 (13909, 13910)	Novel Protein sim. GBank gi 3420605 gb AAC31904.1 - (AF075709) putative sulfonate binding protein precursor [Pseudomonas putida]		UNCLASSIFIED	1003
3875	70947186 (16505, 16506)	Novel Protein sim. GBank gi 3426176 dbj BAA32403 - (AB008771) beta-N- Acetylglucosaminidase [Streptomyces thermophilaceus]		UNCLASSIFIED	1029
3876	56333142 (12839, 12840)	Novel Protein sim. GBank gi 3449110 emb CAA20016 - (AL031130) 1- evidence=predicted by content; 1- method=genefinder;084; 1-method_score=257.34; 1-evidence_end; 2-evidence=predicted by motif; 2- match_accession=PROSITE:PS00343; 2- match_description=Gram-positive cocci surface prote...		UNCLASSIFIED	1046
3877	13070840 (21591, 21592)	Novel Protein sim. GBank gi 3449249 emb CAA20393 - (AL031317) putative integral membrane protein [Streptomyces coelicolor]		UNCLASSIFIED	1024
3878	54994566 (11757, 11758)	Novel Protein sim. GBank gi 3449267 emb CAA20411 - (AL031317) putative transcriptional regulator [Streptomyces coelicolor]		UNCLASSIFIED	1029

3879	80071696 (8863, 8864)	Novel Protein sim. GBank gi 3449270 emb CAA20414 - (AL031317) hypothetical protein SC6G4.36c [Streptomyces coelicolor]		UNCLASSIFIED	1022, 1023, 1031, 1034, 1039, 1053
3880	56333082 (2857, 2858)	Novel Protein sim. GBank gi 3449294 dbj BAA32462 - (AB011532) MEGF8 [Rattus norvegicus]		UNCLASSIFIED	1046
3881	80194752 (3119, 3120)	Novel Protein sim. GBank gi 3451473 emb CAA20490.1 - (AL031349) 4-nitrophenylphosphatase [Schizosaccharomyces pombe]		UNCLASSIFIED	1003, 1004, 1006, 1008, 1022, 1034
3882	36625429 (1073, 1074)	Novel Protein sim. GBank gi 345752 pir S29028 - aspartate transaminase (EC 2.6.1.1) (clone 8C7) - human		UNCLASSIFIED	1034
3883	18598551 (18809, 18810)	Novel Protein sim. GBank gi 346712 pir JC1456 - gelatinase B (EC 3.4.24.35) precursor - mouse		UNCLASSIFIED	1023
3884	80221530 (16527, 16528)	Novel Protein sim. GBank gi 347493 (L22072) - PET112 protein [Saccharomyces cerevisiae]		UNCLASSIFIED	1003, 1022, 1023, 1024, 1025, 1027, 1038
3885	16367942 (4429, 4430)	Novel Protein sim. GBank gi 3482880 (U63816) - unknown protein [Pseudomonas aeruginosa]		UNCLASSIFIED	1003
3886	11696124 (20807, 20808)	Novel Protein sim. GBank gi 3482881 (U63816) - unknown [Pseudomonas aeruginosa]		UNCLASSIFIED	1034
3887	13526199 (14681, 14682)	Novel Protein sim. GBank gi 348415 pir S29383 - hisH protein - Zymomonas mobilis		UNCLASSIFIED	1027
3888	95010016 (17211, 17212)	Novel Protein sim. GBank gi 3493654 (AF083219) - transcription activator [Azospirillum brasilense]		UNCLASSIFIED	1044
3889	7523998 (1643, 1644)	Novel Protein sim. GBank gi 3510505 (AF030881) - pol polyprotein [Fugu rubripes]		UNCLASSIFIED	1058
3890	79820994 (7385, 7386)	Novel Protein sim. GBank gi 3510629 (AF047828) - syringomycin synthetase [Pseudomonas syringae pv. syringae]		UNCLASSIFIED	1039

3891	65480226 (5421, 5422)	Novel Protein sim. GBank gi 3550592 emb CAA08650 - (AJ005645) sdrc [Staphylococcus aureus]		UNCLASSIFIED	1054
3892	78896598 (21241, 21242)	Novel Protein sim. GBank gi 3550592 emb CAA08650 - (AJ005645) sdrc [Staphylococcus aureus]		UNCLASSIFIED	1008, 1016, 1038, 1039
3893	79604379 (12703, 12704)	Novel Protein sim. GBank gi 3551791 emb AF047823 - cyclic beta 1-2 glucan synthetase [Brucella abortus]		UNCLASSIFIED	1034
3894	79555424 (7167, 7168)	Novel Protein sim. GBank gi 3559993 emb CAA20615 - (AL031515) putative transcriptional regulator [Streptomyces coelicolor]		UNCLASSIFIED	1038
3895	80985550 (7677, 7678)	Novel Protein sim. GBank gi 3599940 emb AF017368 - faciogenital dysplasia protein 2 [Mus musculus]		UNCLASSIFIED	1022, 1025
3896	27846167 (1811, 1812)	Novel Protein sim. GBank gi 3638957 emb AC004877 - sco-spondin-mucin-like; similar to P98167 (PID:gi1711548); details of intron/exon structure uncertain [Homo sapiens]		UNCLASSIFIED	1022, 1034
3897	85809924 (3047, 3048)	Novel Protein sim. GBank gi 3641340 gb AAC36351 - (AF090329) cyclohexanone monooxygenase homolog [Pseudomonas fluorescens]		UNCLASSIFIED	1038
3898	27837618 (9453, 9454)	Novel Protein sim. GBank gi 3641337 emb CAA18824.1 - (AL023094) Nonclathrin coat protein gamma-like protein [Arabidopsis thaliana]		UNCLASSIFIED	1010, 1022
3899	27807038 (9939, 9940)	Novel Protein sim. GBank gi 3649748 emb CAA09618 - (AJ011416) IgG Fc binding protein [Mus musculus]		UNCLASSIFIED	1004, 1024
3900	17260914 (15273, 15274)	Novel Protein sim. GBank gi 3660469 emb CAA05024 - (AJ001808) succinyl- CoA-ligase beta subunit [Arabidopsis thaliana]		UNCLASSIFIED	1039
3901	39517841 (21683, 21684)	Novel Protein sim. GBank gi 3676693 emb AF083949 - DNA polymerase; DnaE [Treponema denticola]		UNCLASSIFIED	1006

3902	9217916 (21699, 21700)	Novel Protein sim. GBank gi 3688350 emb CAA19741.1 - (AL030996) dJ1189B24.4 (novel PUTATIVE protein similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8) [Homo sapiens]		UNCLASSIFIED	1022
3903	36732739 (3837, 3838)	Novel Protein sim. GBank gi 3695025 (AF056031) - kynurenine 3-hydroxylase [Rattus norvegicus]		UNCLASSIFIED	1008, 1026
3904	20732929 (1895, 1896)	Novel Protein sim. GBank gi 3721912 dbj BAA33743.1 - (AB017156) gob-5 [Mus musculus]		UNCLASSIFIED	1024
3905	20720703 (8101, 8102)	Novel Protein sim. GBank gi 3724326 dbj BAA33615.1 - (AB012956) unknown [Vibrio cholerae]		UNCLASSIFIED	1006
3906	78989267 (14333, 14334)	Novel Protein sim. GBank gi 3732 emb CAA30693 - (X07846) GCD1 gene product (AA 1 - 511) [Saccharomyces cerevisiae]		UNCLASSIFIED	1017, 1039
3907	11076524 (10745, 10746)	Novel Protein sim. GBank gi 3748666 (AF076848) - trihydroxytoluene oxygenase [Burkholderia cepacia]		UNCLASSIFIED	1010
3908	17930861 (9667, 9668)	Novel Protein sim. GBank gi 3747107 (AF095741) - unknown [Rattus norvegicus]		UNCLASSIFIED	1023
3909	80027058 (13771, 13772)	Novel Protein sim. GBank gi 3757569 emb CAA21315 - (AL031863) 1 - evidence=predicted by content; 1 - method=genefinder;084; 1-method_score=66.31; 1-evidence_end [Drosophila melanogaster]		UNCLASSIFIED	1006, 1029
3910	79751800 (18095, 18096)	Novel Protein sim. GBank gi 3766365 emb CAA21417 - (AL031907) putative cystine-rich transcriptional regulator [Schizosaccharomyces pombe]		UNCLASSIFIED	1004
3911	78759865 (12875, 12876)	Novel Protein sim. GBank gi 3777596 (AF095791) - TACC2 protein [Homo sapiens]		UNCLASSIFIED	1008, 1022

3912	20459875 (18239, 18240)	Novel Protein sim. GBank gij3786001 (AC005499) - unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	1024
3913	25236760 (9091, 9092)	Novel Protein sim. GBank gij3800830[gb AAC6885] - (AF078779) putative four repeat ion channel [Rattus norvegicus]	UNCLASSIFIED	1003
3914	28308249 (19957, 19958)	Novel Protein sim. GBank gij3808292 (AF072440) - GTPase [Enterobacter gergoviae]	UNCLASSIFIED	1003
3915	36996223 (8657, 8658)	Novel Protein sim. GBank gij3810873[dbj BAA34062] - (AB010465) lactonohydrolase [Fusarium oxysporum]	UNCLASSIFIED	1001
3916	9723920 (5019, 5020)	Novel Protein sim. GBank gij3820484 (AF034373) - ataxin-2-like protein A2LP [Homo sapiens]	UNCLASSIFIED	1038, 1039
3917	24109075 (1663, 1664)	Novel Protein sim. GBank gij3822036 (AF072326) - endo-1,3-1,4-beta-D-glucanase [Zea mays]	UNCLASSIFIED	1053
3918	19858634 (4073, 4074)	Novel Protein sim. GBank gij3850084[emb CAA2191.1] - (AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]	UNCLASSIFIED	1034
3919	34394260 (19085, 19086)	Novel Protein sim. GBank gij3850152[emb CAA21952] - (AL033396) hypothetical protein [Candida albicans]	UNCLASSIFIED	1026
3920	13089085 (16051, 16052)	Novel Protein sim. GBank gij3851545[gb AAC72350] - (AF079234) MreB [Vibrio cholerae]	UNCLASSIFIED	1027
3921	78519203 (21779, 21780)	Novel Protein sim. GBank gij3851632 (AF097723) - hematopoietic lineage switch 2 related protein [Rattus norvegicus]	UNCLASSIFIED	1003
3922	78488067 (3555, 3556)	Novel Protein sim. GBank gij3860635[emb CAA14536] - (AJ235270) ARGINYL-TRNA SYNTHETASE (argS) [Rickettsia prowazekii]	UNCLASSIFIED	1039

3923	10053411 (20627, 20628)	Novel Protein sim. GBank gi 3860646 emb CAA14547 - (AJ235270) unknown [Rickettsia prowazekii]		UNCLASSIFIED	1017
3924	17940086 (873, 874)	Novel Protein sim. GBank gi 3860724 emb CAA14625 - (AJ235270) MULTIDRUG RESISTANCE PROTEIN B (emrB) [Rickettsia prowazekii]		UNCLASSIFIED	1039
3925	77520608 (21341, 21342)	Novel Protein sim. GBank gi 3860930 emb CAA14830 - (AJ235271) LYSYL- tRNA SYNTHETASE (lysS) [Rickettsia prowazekii]		UNCLASSIFIED	1023, 1049
3926	9845477 (15603, 15604)	Novel Protein sim. GBank gi 3861105 emb CAA15006 - (AJ235272) unknown [Rickettsia prowazekii]		UNCLASSIFIED	1023
3927	24114042 (9291, 9292)	Novel Protein sim. GBank gi 3861107 emb CAA15007 - (AJ235272) unknown [Rickettsia prowazekii]		UNCLASSIFIED	1044
3928	13041883 (8661, 8662)	Novel Protein sim. GBank gi 3861335 emb CAA15235 - (AJ235273) unknown [Rickettsia prowazekii]		UNCLASSIFIED	1024
3929	66556191 (9465, 9466)	Novel Protein sim. GBank gi 3861430 emb CAA22035 - (AL033505) hypothetical protein SC1E6.07 [Streptomyces coelicolor]		UNCLASSIFIED	1023
3930	80048280 (18469, 18470)	Novel Protein sim. GBank gi 3861444 emb CAA22049 - (AL033505) ABC transporter ATP-binding protein [Streptomyces coelicolor]		UNCLASSIFIED	1004, 1034, 1039
3931	20212376 (14801, 14802)	Novel Protein sim. GBank gi 3868935 dbj BAA34293 - (AB015023) MurC [Corynebacterium glutamicum]		UNCLASSIFIED	1010
3932	20727907 (5881, 5882)	Novel Protein sim. GBank gi 3868940 dbj BAA34296 - (AB015054) Alg2 [Rhizomucor pusillus]		UNCLASSIFIED	1006

3933	9868440 (3663, 3664)	Novel Protein sim. GBank gil3873550 emb CAA221271 - (AL033534) serine-rich protein [Schizosaccharomyces pombe]		UNCLASSIFIED	1008
3934	23333239 (4121, 4122)	Novel Protein sim. GBank gil3873550 emb CAA221271 - (AL033534) serine-rich protein [Schizosaccharomyces pombe]		UNCLASSIFIED	1053
3935	79585543 (6257, 6258)	Novel Protein sim. GBank gil3875537 emb CAA91320.1 - (Z66511) similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST CEMSA01F comes from this gene; cDNA EST CEMSA01R comes from this gene; cDNA EST EMBL:T01268 comes from this gene; cDNA EST EMBL:D37044 comes f...		UNCLASSIFIED	1054
3936	23299986 (6807, 6808)	Novel Protein sim. GBank gil3875521 emb CAB04059 - (Z81495) predicted using Genefinder [Caenorhabditis elegans]		UNCLASSIFIED	1044
3937	94146710 (17179, 17180)	Novel Protein sim. GBank gil3875726 emb CAA91030 - (Z54270) similar to nir like gene involved in denitrification; cDNA EST EMBL:D27430 comes from this gene; cDNA EST EMBL:D27432 comes from this gene; cDNA EST EMBL:D27431 comes from this gene; cDNA EST EMBL:D33667 comes from thi...		UNCLASSIFIED	1003
3938	55474436 (4305, 4306)	Novel Protein sim. GBank gil3877422 emb CAB05195.1 - (Z82268) predicted using Genefinder; similar to CUTICLE COLLAGEN 34; cDNA EST EMBL:D65629 comes from this gene; cDNA EST EMBL:D68754 comes from this gene; cDNA EST EMBL:D68791 comes from this gene; cDNA EST EMBL:D68988 comes ...		UNCLASSIFIED	1026

3939	79574578 (2511, 2512)	Novel Protein sim. GBank gij3877738[emb]CAA98949 - (Z74473) predicted using GeneFinder [Caenorhabditis elegans]	UNCLASSIFIED	1031
3940	27361342 (8423, 8424)	Novel Protein sim. GBank gij3881524[emb]CAA93883 - (Z70038) ZK1067.4 [Caenorhabditis elegans]	UNCLASSIFIED	1023
3941	87454308 (21791, 21792)	Novel Protein sim. GBank gij3881976[emb]CAA10008 - (AJ012409) hypothetical protein [Homo sapiens]	UNCLASSIFIED	1025
3942	66489815 (5441, 5442)	Novel Protein sim. GBank gij3882185[dbj]BAA34452.1 - (AB018275) KIAA0732 protein [Homo sapiens]	UNCLASSIFIED	1029
3943	8502066 (21961, 21962)	Novel Protein sim. GBank gij3885988 (AF103809) - Ap-3 complex beta3A subunit [Mus musculus]	UNCLASSIFIED	1024
3944	5472309 (18139, 18140)	Novel Protein sim. GBank gij3894172 (AC005312) - putative cinnamoyl-CoA reductase [Arabidopsis thaliana]	UNCLASSIFIED	1058
3945	20697087 (6089, 6090)	Novel Protein sim. GBank gij3901272 (AF067656) - ZW10 interactor Zwint [Homo sapiens]	UNCLASSIFIED	1034, 1058
3946	30506233 (13837, 13838)	Novel Protein sim. GBank gij3901272 (AF067656) - ZW10 interactor Zwint [Homo sapiens]	UNCLASSIFIED	1009
3947	95292917 (20971, 20972)	Novel Protein sim. GBank gij3913029[sp]P94967 ALR_MYCSM - ALANINE RACEMASE	UNCLASSIFIED	1010, 1024, 1034
3948	80502395 (22699, 22700)	Novel Protein sim. GBank gij3913089[sp]P94992 ARGR_MYCTU - PROBABLE ARGININE REPRESSOR	UNCLASSIFIED	1012
3949	79763719 (19661, 19662)	Novel Protein sim. GBank gij3913102[sp]O50175 ASTB_PSEAE - SUCCINYLARGININE DIHYDROLASE	UNCLASSIFIED	1008
3950	11099897 (22549, 22550)	Novel Protein sim. GBank gij3913585[sp]O69162 ERA_BRAJA - GTP- BINDING PROTEIN ERA HOMOLOG	UNCLASSIFIED	1006

3951	79830615 (16681, 16682)	Novel Protein sim. GBank gil3914254 sp O06875 P39_BRUAB - IMMUNOGENIC 39 KD PROTEIN		UNCLASSIFIED	1039
3952	87112829 (1471, 1472)	Novel Protein sim. GBank gil3914489 sp O32333 PTHB_CLOBE - PTS SYSTEM, GLUCITOL/SORBITOL-SPECIFIC IIBC COMPONENT (EIIIC-GUT) (GLUCITOL/SORBITOL-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EII-GUT)		UNCLASSIFIED	1008, 1018, 1026
3953	10103453 (14839, 14840)	Novel Protein sim. GBank gil3915143 sp O31741 TRMD_BACSU - TRNA (GUANINE-N1)-METHYLTRANSFERASE (M1G-METHYLTRANSFERASE) (TRNA [GM37] METHYLTRANSFERASE)		UNCLASSIFIED	1012
3954	11776548 (10509, 10510)	Novel Protein sim. GBank gil3913407 sp O58584 YA28_PYRHO - HYPC1 HETICAL PROTEIN PHAL028		UNCLASSIFIED	1022
3955	79487814 (4843, 4844)	Novel Protein sim. GBank gil3915450 sp P76270 YEER_ECOLI - HYPOTHETICAL 20.3 KD PROTEIN IN PRC-PPHA INTERGENIC REGION		UNCLASSIFIED	1006
3956	80027421 (18883, 18884)	Novel Protein sim. GBank gil3915488 sp O34961 YJMB_BACSU - HYPOTHETICAL SYMPORTER IN COTT-RAPA INTERGENIC REGION		UNCLASSIFIED	1006, 1016, 1022, 1027, 1034, 1039
3957	79837693 (8737, 8738)	Novel Protein sim. GBank gil3915493 sp O68826 YIGM_PSEAE - HYPOTHETICAL 31.7 KD PROTEIN IN PHEC-RARD INTERGENIC REGION		UNCLASSIFIED	1008
3958	10249385 (5921, 5922)	Novel Protein sim. GBank gil3915570 sp O34553 YTSP_BACSU - HYPOTHETICAL 8.7 KD PROTEIN IN BRAB-RPSD INTERGENIC REGION		UNCLASSIFIED	1023

3959	80488988 (13693, 13694)	Novel Protein sim. GBank gi 3915659 sp Q10671 COBL_MYCTU - PRECORRIN-6Y C5,15-METHYLTRANSFERASE [DECARBOXYLATING] (PRECORRIN-6 METHYLTRANSFERASE) (PRECORRIN-6Y METHYLASE)		UNCLASSIFIED	1001, 1004, 1006, 1010, 1012, 1017, 1026, 1027, 1031, 1034, 1039, 1044
3960	20617394 (18129, 18130)	Novel Protein sim. GBank gi 3915993 sp P76250 YEAT_ECOLI - HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN GAPA-RND INTERGENIC REGION		UNCLASSIFIED	1004
3961	79612824 (10109, 10110)	Novel Protein sim. GBank gi 3924708 emb CAA84646 - (Z35597) Weak similarity with sea squirt nidogen precursor protein (blastp score 71); cDNA EST EMBL:T02069 comes from this gene; cDNA EST EMBL:D76135 comes from this gene; cDNA EST EMBL:D73147 comes from this gene; cDNA EST EMB...		UNCLASSIFIED	1022
3962	78499068 (7771, 7772)	Novel Protein sim. GBank gi 3928150 emb CAA10289 - (AJ131049) hypothetical protein [Cicer arietinum]		UNCLASSIFIED	1016
3963	79868855 (16225, 16226)	Novel Protein sim. GBank gi 3928723 emb CAA22219 - (AL034355) putative ABC transporter [Streptomyces coelicolor]		UNCLASSIFIED	1029, 1038
3964	80080052 (2403, 2404)	Novel Protein sim. GBank gi 3928904 (AF104259) - D-lysine 5,6-aminomutase alpha subunit [Clostridium sticklandii]		UNCLASSIFIED	1026, 1029, 1034, 1053
3965	78505129 (22979, 22980)	Novel Protein sim. GBank gi 3929019 (AF057695) - putative phosphomannomutase [Haemophilus ducreyi]		UNCLASSIFIED	1022
3966	5731182 (17825, 17826)	Novel Protein sim. GBank gi 3935181 (AC004557) - F17L21.24 [Arabidopsis thaliana]		UNCLASSIFIED	1058

3967	11348438 (19659, 19660)	Novel Protein sim. GBank gi 3953516 dbj BAA34717 - (AB002529) sensor kinase rtpA [Pseudomonas tolaasii]	UNCLASSIFIED	1034
3968	39990483 (11115, 11116)	Novel Protein sim. GBank gi 3955013 emb CAA09105 - (AJ010393) hypotrifical protein [Pseudomonas oleovorans]	UNCLASSIFIED	1016
3969	78723682 (269, 270)	Novel Protein sim. GBank gi 3978464 (AF085693) - G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein [Rattus norvegicus]	UNCLASSIFIED	1030
3970	23329490 (4905, 4906)	Novel Protein sim. GBank gi 3978488 (AF082918) - virulence regulating homolog [Pseudomonas alcaligenes]	UNCLASSIFIED	1026
3971	39996970 (12591, 12592)	Novel Protein sim. GBank gi 3980411 (AC004561) - putative proline-rich protein [Arabidopsis thaliana]	UNCLASSIFIED	1001
3972	27976344 (9353, 9354)	Novel Protein sim. GBank gi 3986770 (AF109906) - NG2 ? [Mus musculus]	UNCLASSIFIED	1024
3973	78913805 (18075, 18076)	Novel Protein sim. GBank gi 399006 sp Q02336 ADA2_YEAST - POTENTIAL TRANSCRIPTIONAL ADAPTOR	UNCLASSIFIED	1044
3974	66398162 (15901, 15902)	Novel Protein sim. GBank gi 399378 sp P31080 LEXA_BACSU - SOS REGULATORY PROTEIN LEXA/DINR	UNCLASSIFIED	1008
3975	79470555 (18283, 18284)	Novel Protein sim. GBank gi 399980 sp P28155 HYPB_RHILV - HYDROGENASE EXPRESSION/FORMATION PROTEIN HYPB	UNCLASSIFIED	1022
3976	29018958 (8735, 8736)	Novel Protein sim. GBank gi 400052 sp Q02138 LVC_LACLA - KETOL-ACID REDUCTOISOMERASE (ACETOHYDROXY-ACID ISOMEROREDUCTASE) (ALPHA-KETO-BETA-HYDROXYLACIL REDUCTOISOMERASE)	UNCLASSIFIED	1017
3977	20711888 (20917, 20918)	Novel Protein sim. GBank gi 400324 sp P31179 NADA_CYAPA - QUINOLINATE SYNTHETASE A	UNCLASSIFIED	1022

3978	27823479 (9323, 9324)	Novel Protein sim. GBank gil400663 sp P31755 OCH1_YEAST - ALPHA-1,6-MANNOSYLTRANSFERASE		UNCLASSIFIED	1004, 1022, 1024, 1034
3979	80439852 (17195, 17196)	Novel Protein sim. GBank gil4007681 emb CAA22367 - (AL034443) putative integral membrane transporter [Streptomyces coelicolor]		UNCLASSIFIED	1038
3980	65469531 (21673, 21674)	Novel Protein sim. GBank gil4007726 emb CAA22410 - (AL034447) putative methylase [Streptomyces coelicolor]		UNCLASSIFIED	1008
3981	78923067 (11683, 11684)	Novel Protein sim. GBank gil4007736 emb CAA22420 - (AL034447) putative chromosome associated protein [Streptomyces coelicolor]		UNCLASSIFIED	1017
3982	25259598 (14463, 14464)	Novel Protein sim. GBank gil4007738 emb CAA22422 - (AL034447) putative transmembrane protein [Streptomyces coelicolor]		UNCLASSIFIED	1008
3983	78367994 (35, 36)	Novel Protein sim. GBank gil4008343 emb CAB16307.1 - (Z99169) C26H9A_2 [Caenorhabditis elegans]		UNCLASSIFIED	1003
3984	65680443 (781, 782)	Novel Protein sim. GBank gil401469 sp P28635 YAEC_ECOLI - HYPOTHETICAL 29.4 KD LIPOPROTEIN IN RCSF-ABC INTERGENIC REGION PRECURSOR		UNCLASSIFIED	1041
3985	78326497 (2677, 2678)	Novel Protein sim. GBank gil401521 sp Q01334 YCR3_ERWHE - HYPOTHETICAL 29.9 KD PROTEIN IN CRTE 3'REGION (ORF3)		UNCLASSIFIED	1039
3986	79485919 (18921, 18922)	Novel Protein sim. GBank gil403171 (L24492) - ethanolamine ammonia-lyase large subunit [Rhodococcus erythropolis]		UNCLASSIFIED	1022
3987	80080258 (549, 550)	Novel Protein sim. GBank gil4033729 (AF038595) - apolipoprotein N-acyltransferase [Pseudomonas aeruginosa]		UNCLASSIFIED	1027, 1031, 1034

3988	32420106 (16625, 16626)	Novel Protein sim. GBank gjl403406 (U00100) - unknown [Pseudomonas aeruginosa]	UNCLASSIFIED	1029
3989	85543977 (21461, 21462)	Novel Protein sim. GBank gjl403460 (L24521) - transylmation-related protein [Homo sapiens]	UNCLASSIFIED	1008, 1030, 1054
3990	78308048 (21147, 21148)	Novel Protein sim. GBank gjl404524 [bbs]136180 - (S64520) pyruvate: ferredoxin oxidoreductase [Anabaena variabilis, Peptide Partial, 91 aa]	UNCLASSIFIED	1026
3991	16316610 (18763, 18764)	[Anabaena variabilis]	UNCLASSIFIED	1001
3992	80027600 (7055, 7056)	Novel Protein sim. GBank suppressor [Saccharomyces cerevisiae]	UNCLASSIFIED	1004, 1006, 1009, 1023, 1038
3993	20629923 (6413, 6414)	Novel Protein sim. GBank gjl4049524 [emb]CAA10483] - (AJ131707) fructose 1,6-bisphosphate aldolase [Streptomyces galbus]	UNCLASSIFIED	1010
3994	78758003 (18967, 18968)	Novel Protein sim. GBank gjl405655 [emb]CAA22586] - (AL034583) putative elongation initiation factor subunit [Schizosaccharomyces pombe]	UNCLASSIFIED	1030
3995	79245937 (1369, 1370)	Novel Protein sim. GBank gjl405895 (U00007) - methionyl-tRNA synthetase [Escherichia coli]	UNCLASSIFIED	1039
3996	17939614 (309, 310)	Novel Protein sim. GBank gjl4062973 [dbj]BAA36204.1] - (AB017138) alpha subunit of malonate decarboxylase [Pseudomonas putida]	UNCLASSIFIED	1039
3997	5631925 (22675, 22676)	Novel Protein sim. GBank gjl4092859 (AF033120) - p53 regulated PA26-T2 nuclear protein [Homo sapiens]	UNCLASSIFIED	1058
3998	56001677 (4235, 4236)	Novel Protein sim. GBank gjl4098081 (U73336) - anaerobic ribonucleotide reductase [Lactococcus lactis]	UNCLASSIFIED	1003
3999	11635413 (1851, 1852)	Novel Protein sim. GBank gjl4104762 [gb]AAD02144.1] - (AF039534) transposase-like protein TrpA2 [Pseudomonas stutzeri]	UNCLASSIFIED	1006

4000	79761420 (11707, 11708)	Novel Protein sim. GBank gjl4104925 (AF042276) - poly(hydroxycanoate) granule associated protein CAA2 [Pseudomonas putida]	UNCLASSIFIED	1001, 1008
4001	79398200 (20263, 20264)	Novel Protein sim. GBank gjl4106577[emb]CAA21332] - (AL031866) ORF10, len: 268 aa, hutG, highly similar to N-formylglutamate amidohydrolase from Pseudomonas putida AF032970_3, Fasta scores: opt: 1057, E(): 0, 59.6% identity in 260 aa overlap [Yersinia pestis]	UNCLASSIFIED	1006
4002	81809267 (617, 618)	Novel Protein sim. GBank gjl4106587[emb]CAA21342] - (AL031866) ORF19, len: 473 aa, similar to tyrosine aminotransferase, highly similar to E. coli D90784_2, Fasta scores opt:1842, E(): 0 [Yersinia pestis]	UNCLASSIFIED	1012, 1054
4003	36827630 (5481, 5482)	Novel Protein sim. GBank gjl4106610[emb]CAA21365] - (AL031866) ORF42, len=386 aa, similarity to an aminotransferase, in P95957 Sulfolobus solfataricus, (401 aa), 33.1% identity in 393 aa overlap, Fasta scores: opt:468, E(): 8.5e-24, in Q64602 R. norvegicus, (425 aa), 28.6% ident...	UNCLASSIFIED	1054
4004	79489610 (19187, 19188)	Novel Protein sim. GBank gjl4106613[emb]CAA21368] - (AL031866) ORF45, len= 289 aa, unknown [Yersinia pestis]	UNCLASSIFIED	1022
4005	10812585 (14111, 14112)	Novel Protein sim. GBank gjl4115383 (AC005967) - receptor-like protein kinase [Arabidopsis thaliana]	UNCLASSIFIED	1034
4006	14995389 (16631, 16632)	Novel Protein sim. GBank gjl4115511[dbj]BAA36399.1] - (AB010947) FltY [Salmonella typhimurium]	UNCLASSIFIED	1024
4007	79846253 (12761, 12762)	Novel Protein sim. GBank gjl4115631[dbj]BAA36469] - (AB015053) ORFX; unassigned reading frame [Pseudomonas fluorescens]	UNCLASSIFIED	1039

4008	79249976 (1921, 1922)	Novel Protein sim. GBank gi 4128215 (AF095748) - putative phthalate permease C-terminal region [Burkholderia cepacia]		UNCLASSIFIED	1001
4009	79610551 (4565, 4566)	Novel Protein sim. GBank gi 4154082 emb CAA22735 - (AL035161) putative aminoacylase [Streptomyces coelicolor]		UNCLASSIFIED	1004, 1041
4010	91014288 (1491, 1492)	Novel Protein sim. GBank gi 4155340 (AE001508) - TYPE I RESTRICTION ENZYME (RESTRICTION SUBUNIT) [Helicobacter pylori J99]		UNCLASSIFIED	1010
4011	66376543 (10897, 10898)	Novel Protein sim. GBank gi 4155544 (AE001525) - putative POLYSACCHARIDE BIOSYNTHESIS PROTEIN [Helicobacter pylori J99]		UNCLASSIFIED	1009, 1010
4012	80209497 (11793, 11794)	Novel Protein sim. GBank gi 4155633 (AE001532) - putative [Helicobacter pylori J99]		UNCLASSIFIED	1034
4013	10857039 (325, 326)	Novel Protein sim. GBank gi 4155750 (AE001542) - D-LACTATE DEHYDROGENASE [Helicobacter pylori J99]		UNCLASSIFIED	1006
4014	80209512 (16981, 16982)	Novel Protein sim. GBank gi 4155868 (AE001549) - putative TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE [Helicobacter pylori J99]		UNCLASSIFIED	1034
4015	13886417 (15477, 15478)	Novel Protein sim. GBank gi 4155870 (AE001549) - putative [Helicobacter pylori J99]		UNCLASSIFIED	1053
4016	14218589 (12173, 12174)	Novel Protein sim. GBank gi 4155916 (AE001554) - lipopolysaccharide biosynthesis protein [Helicobacter pylori J99]		UNCLASSIFIED	1053
4017	79107407 (14345, 14346)	Novel Protein sim. GBank gi 4156196 (AC004865) - similar to KIAA0319; similar to AB002317 (PID:g2224579) [Homo sapiens]		UNCLASSIFIED	1023
4018	25267792 (3601, 3602)	Novel Protein sim. GBank gi 4160312 emb CAA22763 - (AL035212) hypothetical protein SC9B2.03 [Streptomyces coelicolor]		UNCLASSIFIED	1003

4019	20753820 (17145, 17146)	Novel Protein sim. GBank gil416583 sp P27550 ACSA_ECOLI - ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)		UNCLASSIFIED	1004
4020	80235985 (1607, 1608)	Novel Protein sim. GBank gil416592 sp P32323 AGA1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR		UNCLASSIFIED	1006, 1023
4021	85806685 (16071, 16072)	Novel Protein sim. GBank gil416592 sp P32323 AGA1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR		UNCLASSIFIED	1017, 1019, 1026, 1053, 1054
4022	79611262 (2165, 2166)	Novel Protein sim. GBank gil416761 sp P32468 CC12_YEAST - CELL DIVISION CONTROL PROTEIN 12 (SEPTIN)		UNCLASSIFIED	1001, 1006, 1044
4023	80227710 (21228, 21230)	Novel Protein sim. GBank gil417039 sp Q01722 GCR2_YEAST - GLYCOLYTIC GENES TRANSCRIPTIONAL ACTIVATOR GCR2		UNCLASSIFIED	1006, 1022, 1034
4024	65454473 (11741, 11742)	Novel Protein sim. GBank gil417226 sp P32895 KPR1_YEAST - RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 1 (PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 1)		UNCLASSIFIED	1016, 1022
4025	47652453 (12005, 12006)	Novel Protein sim. GBank gil417315 sp P32653 MRP_STRSU - MURAMIDASE-RELEASED PROTEIN PRECURSOR (136 KD SURFACE PROTEIN)		UNCLASSIFIED	1029
4026	78728488 (9511, 9512)	Novel Protein sim. GBank gil417457 sp P32767 PDR6_YEAST - PLEIOTROPIC DRUG RESISTANCE REGULATORY PROTEIN 6		UNCLASSIFIED	1008, 1009, 1017, 1022, 1026, 1039, 1044
4027	25262406 (12921, 12922)	Novel Protein sim. GBank gil4176522 emb CAA22878 - (AL035263) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	1008

4028	95292770 (21553, 21654)	Novel Protein sim. GBank gil417770 sp P32432 SFP1_YEAST - ZINC FINGER PROTEIN SFP1		UNCLASSIFIED	1004
4029	80219785 (5281, 5282)	Novel Protein sim. GBank gil417778 sp P32908 SMC1_YEAST - CHROMOSOME SEGREGATION PROTEIN SMC1 (DA-BOX PROTEIN SMC1)		UNCLASSIFIED	1004, 1006, 1008, 1010, 1024, 1027, 1031
4030	30660836 (12051, 12052)	Novel Protein sim. GBank gil417826 sp P32579 SUA5_YEAST - SUA5 PROTEIN		UNCLASSIFIED	1026
4031	37798306 (12211, 12212)	Novel Protein sim. GBank gil418384 sp P32057 WCAI_ECOLI - PUTATIVE COLANIC ACID BIOSYNTHESIS GLYCOSYL TRANSFERASE WCAI		UNCLASSIFIED	1012
4032	29449853 (21729, 21730)	Novel Protein sim. GBank gil418427 sp P32634 YEW2_YEAST - HYPOTHETICAL 195.4 KD PROTEIN IN RPS26B- GLC7 INTERGENIC REGION		UNCLASSIFIED	1026
4033	80042837 (5815, 5816)	Novel Protein sim. GBank gil418488 sp P32147 YHZ_ECOLI - HYPOTHETICAL 15.9 KD PROTEIN IN RBN- FDHE INTERGENIC REGION (O145)		UNCLASSIFIED	1053
4034	9383442 (9203, 9204)	Novel Protein sim. GBank gil418501 sp P32159 YIIP_ECOLI - HYPOTHETICAL 32.9 KD PROTEIN IN CPXA- PFKA INTERGENIC REGION		UNCLASSIFIED	1017
4035	8490783 (2585, 2586)	Novel Protein sim. GBank gil418572 sp P32882 YKD8_YEAST - PUTATIVE 128.2 KD TRANSCRIPTIONAL REGULATORY PROTEIN IN PTM1-XR1 INTERGENIC REGION		UNCLASSIFIED	1024
4036	56149063 (7345, 7346)	Novel Protein sim. GBank gil418600 sp P32792 YHH7_YEAST - HYPOTHETICAL 44.2 KD PROTEIN IN SPO13- ARG4 INTERGENIC REGION		UNCLASSIFIED	1003

4037	30198359 (7755, 7756)	Novel protein sim. GBank gi 419481 pir A46312 - gag polyprotein - human endogenous virus S71	UNCLASSIFIED	1026
4038	38615868 (4941, 4942)	Novel Protein sim. GBank gi 419757 pir S30145 - ketol-acid reductoisomerase (EC 1.1.1.86) precursor - Arabidopsis thaliana	UNCLASSIFIED	1008, 1025
4039	94664584 (22829, 22830)	Novel Protein sim. GBank gi 419857 pir S34027 - CDC47 protein - yeast (<i>Saccharomyces cerevisiae</i>)	UNCLASSIFIED	1010
4040	28786675 (19377, 19378)	Novel Protein sim. GBank gi 4204263 (AC005223) - 40409 [Arabidopsis thaliana]	UNCLASSIFIED	1017
4041	94233665 (18313, 18314)	Novel Protein sim. GBank gi 4204265 (AC005223) - 45643 [Arabidopsis thaliana]	UNCLASSIFIED	1003, 1004
4042	20024135 (22073, 22074)	Novel Protein sim. GBank gi 4204304 (AC003027) - lclprt_seq No definition line found [Arabidopsis thaliana]	UNCLASSIFIED	1010
4043	10368203 (16661, 16662)	Novel protein sim. GBank gi 4204747 (U49838) - 72.2 kDa protein [Mycobacterium leprae]	UNCLASSIFIED	1008
4044	79207689 (14799, 14800)	Novel protein sim. GBank gi 4206763 (AF104328) - cell wall-plasma membrane linker protein homolog [Arabidopsis thaliana]	UNCLASSIFIED	1001
4045	20724578 (5729, 5730)	Novel protein sim. GBank gi 420945 pir A47041 - transposase homolog (insertion element ISAE1) - <i>Alcaligenes eutrophus</i>	UNCLASSIFIED	1006
4046	17932141 (18111, 18112)	Novel Protein sim. GBank gi 421091 pir S30730 - hypothetical protein o206 - <i>Escherichia coli</i>	UNCLASSIFIED	1023
4047	10887336 (9541, 9542)	Novel Protein sim. GBank gi 42144 emb CAA25200 - (X00513) NusA protein (nusA) [<i>Escherichia coli</i>]	UNCLASSIFIED	1027
4048	87461732 (17329, 17330)	Novel Protein sim. GBank gi 4220517 emb CAA22990 - (AL035356) hypothetical protein [Arabidopsis thaliana]	UNCLASSIFIED	1025

4049	8518032 (21319, 21320)	Novel Protein sim. GBank gil4220523[emb CAA22996] - (AL035356) putative allitin lyase [Arabidopsis thaliana]		UNCLASSIFIED	1022
4050	20294766 (9587, 9588)	Novel Protein sim. GBank gil4234790 (AF078135) - unknown [Leptospira borgpetersenii]		UNCLASSIFIED	1034
4051	29481334 (2687, 2688)	Novel Protein sim. GBank gil423565[pir S34583 - serine proteinase (EC 3.4.21.-) PC6B - mouse		UNCLASSIFIED	1038
4052	10115867 (2855, 2856)	Novel Protein sim. GBank gil4240195[dbj BAA74876.1] - (AB020660) KIAA0853 protein [Homo sapiens]		UNCLASSIFIED	1017
4053	20598367 (13221, 13222)	Novel Protein sim. GBank gil4240195[dbj BAA74876.1] - (AB020660) KIAA0853 protein [Homo sapiens]		UNCLASSIFIED	1022
4054	57291915 (21019, 21020)	Novel Protein sim. GBank gil4240195[dbj BAA74876.1] - (AB020660) KIAA0853 protein [Homo sapiens]		UNCLASSIFIED	1010
4055	78674809 (13125, 13126)	Novel Protein sim. GBank gil4263695[gb AAD1538.1] - (AC006223) putative myosin II heavy chain [Arabidopsis thaliana]		UNCLASSIFIED	1009
4056	29242471 (3935, 3936)	Novel Protein sim. GBank gil4320[emb CAA36300] - (X52081) RGP1 (reduced growth phenotype) gene product (AA 1- 661) [Saccharomyces cerevisiae]		UNCLASSIFIED	1017
4057	11698120 (2559, 2560)	Novel Protein sim. GBank gil4322011[gb AAD15914] - (AF069392) polar flagellar assembly protein [Vibrio parahaemolyticus]		UNCLASSIFIED	1031
4058	55997711 (2417, 2418)	Novel Protein sim. GBank gil432498 (L26506) - ZMS1 [Saccharomyces cerevisiae]		UNCLASSIFIED	1003

4059	28301995 (14845, 14846)	Novel Protein sim. GBank gil4325346 gb AAD17345 - (AF128393) similar to N-ethylmaleimide sensitive fusion proteins; contains similarity to ATPases (Pfam: PF00004, Score=307.7, E=1.4e-88n N=1) [Arabidopsis thaliana]		UNCLASSIFIED	1017
4060	27364469 (18131, 18132)	Novel Protein sim. GBank gil4328 emb CAA47121 - (X66501) RIF1 [Saccharomyces cerevisiae]		UNCLASSIFIED	1022
4061	10858157 (6137, 6138)	Novel Protein sim. GBank gil4336800 gb AAD17959 - (AF106002) toluene tolerance protein Tlg2C [Pseudomonas putida]		UNCLASSIFIED	1031
4062	39710928 (13657, 13658)	Novel Protein sim. GBank gil4337174 gb AAD18095 - (AC006416) Similar to gil1573829 H10816 aminopeptidase P homolog (pepP) from Haemophilus influenzae genome gbU32764. [Arabidopsis thaliana]		UNCLASSIFIED	1026
4063	10174167 (7909, 7910)	Novel Protein sim. GBank gil4371280 gb AAD18138 - (AC006260) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	1004
4064	29685014 (15419, 15420)	Novel Protein sim. GBank gil4376670 gb AAD18535 - (AE001623) dCTP Deaminase [Chlamydia pneumoniae]		UNCLASSIFIED	1038
4065	10331900 (20469, 20470)	Novel Protein sim. GBank gil4377312 gb AAD19121 - (AE001679) Ribonucleoside Reductase, Large Chain [Chlamydia pneumoniae]		UNCLASSIFIED	1003
4066	34868401 (17955, 17956)	Novel Protein sim. GBank gil4388730 gb AAD19768 - (AC006413) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	1034
4067	85528859 (20389, 20390)	Novel Protein sim. GBank gil4406775 gb AAD20086 - (AC006836) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	1049
4068	16395460 (20235, 20236)	Novel Protein sim. GBank gil4416478 gb AAD20378 - (AF125999) transposase [Mycobacterium avium]		UNCLASSIFIED	1017

4069	79202004 (13603, 13604)	Novel Protein sim. GBank gi 4455098 gb AAD21076 - (AF121797) A/G-specific adenine glycosylase [Streptomyces antibioticus]		UNCLASSIFIED	1024
4070	25143281 (15063, 15064)	Novel Protein sim. GBank gi 4455367 emb CAB36777.1 - (AL035524) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	1003
4071	8208833 (18665, 18666)	Novel Protein sim. GBank gi 4455367 emb CAB36777.1 - (AL035524) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	1022
4072	49127474 (10057, 10058)	Novel Protein sim. GBank gi 4455767 emb CAB36883 - (AL035537) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	1040
4073	65691754 (971, 972)	Novel Protein sim. GBank gi 4467126 emb CAB37560 - (AL035538) guanine nucleotide-exchange protein-like [Arabidopsis thaliana]		UNCLASSIFIED	1009
4074	71761719 (1441, 1442)	Novel Protein sim. GBank gi 4467249 emb CAB37574 - (AL035569) probable Glu-tRNA ^{Gln} amidotransferase subunit C [Streptomyces coelicolor]		UNCLASSIFIED	1008, 1026
4075	35904710 (159, 160)	Novel Protein sim. GBank gi 4467252 emb CAB37577 - (AL035569) probable Glu-tRNA ^{Gln} amidotransferase subunit B [Streptomyces coelicolor]		UNCLASSIFIED	1029
4076	33205246 (13817, 13818)	Novel Protein sim. GBank gi 4467252 emb CAB37577 - (AL035569) probable Glu-tRNA ^{Gln} amidotransferase subunit B [Streptomyces coelicolor]		UNCLASSIFIED	1026
4077	80248876 (18671, 18672)	Novel Protein sim. GBank gi 4490579 emb CAB38729.1 - (AJ010302) mg protoporphyrin IX monomethyl ester oxidative cyclase subunit [Rhodobacter sphaeroides]		UNCLASSIFIED	1006, 1022

4078	80173375 (20561, 20562)	Novel Protein sim. GBank gi 4494921 gb AAD21343.1 - (AF083501) capsid protein [Macaca mulatta rhadinovirus 17577]		UNCLASSIFIED	1022
4079	79833783 (11355, 11356)	Novel Protein sim. GBank gi 4502245 ref NP_003967.1 pARTN - neurotrophic factor artemin precursor		UNCLASSIFIED	1008
4080	83220998 (4723, 4724)	Novel Protein sim. GBank gi 4503275 ref NP_001913.1 pDCT - dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2)		UNCLASSIFIED	1028
4081	94673275 (6111, 6112)	Novel Protein sim. GBank gi 4503895 ref NP_000145.1 pGALK - galactokinase 1		UNCLASSIFIED	1031
4082	78389465 (9099, 9100)	Novel Protein sim. GBank gi 4504525 ref NP_003962.1 pHSS - UNKNOWN		UNCLASSIFIED	1008
4083	30577213 (15791, 15792)	Novel Protein sim. GBank gi 4506193 ref NP_002779.1 pPSMA - proteasome (prosome, macropain) subunit, alpha type, 3		UNCLASSIFIED	1009
4084	46892345 (12117, 12118)	Novel Protein sim. GBank gi 4506545 ref NP_002923.1 pRMSA - regulator of mitotic spindle assembly 1		UNCLASSIFIED	1042
4085	78728876 (17701, 17702)	Novel Protein sim. GBank gi 4510347 gb AAD21436.1 - (AC006921) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	1022, 1053
4086	37028586 (14485, 14486)	Novel Protein sim. GBank gi 4511974 gb AAD21534.1 - (AF088896) unknown [Zymomonas mobilis]		UNCLASSIFIED	1038
4087	29354727 (16987, 16988)	Novel Protein sim. GBank gi 4512242 dbj BAA75236.1 - (AB014750) polypeptide [Nicotiana tabacum]		UNCLASSIFIED	1008
4088	79877933 (17547, 17548)	Novel Protein sim. GBank gi 4512377 dbj BAA75341.1 - (AB011837) sorbitol dehydrogenase [Bacillus halodurans]		UNCLASSIFIED	1001, 1003, 1006, 1012, 1017, 1024, 1026, 1027, 1031

4089	35933724 (20725, 20726)	Novel Protein sim. GBank gi 4512492 dbj BAA75141.1 - (AB021078) 100 pct identical to gp:STYINC1PR_5.prf:2209346E[TrbC of plasmid R64] [Plasmid Collb-Pg]		UNCLASSIFIED	1053
4090	21629494 (9909, 9910)	Novel Protein sim. GBank gi 4512671 gb AAD21725.1 - (AC006931) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	1001
4091	20296627 (2717, 2718)	Novel Protein sim. GBank gi 4539105 emb CAB39826.1 - (AL049491) putative ATP-binding protein [Mycobacterium leprae]		UNCLASSIFIED	1034
4092	78787745 (12651, 12652)	Novel Protein sim. GBank gi 4539105 emb CAB39826.1 - (AL049491) putative ATP-binding protein [Mycobacterium leprae]		UNCLASSIFIED	1017, 1049
4093	20727978 (17891, 17892)	Novel Protein sim. GBank gi 4539193 emb CAB39722.1 - (AL049485) putative fatty oxidation protein [Streptomyces coelicolor]		UNCLASSIFIED	1006
4094	20715521 (17865, 17866)	Novel Protein sim. GBank gi 4539223 emb CAB39881.1 - (AL049497) putative integral membrane protein [Streptomyces coelicolor]		UNCLASSIFIED	1022, 1039
4095	23285736 (1515, 1516)	Novel Protein sim. GBank gi 4539292 emb CAB39595.1 - (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]		UNCLASSIFIED	1008
4096	14996508 (6603, 6604)	Novel Protein sim. GBank gi 4539383 emb CAB37449.1 - (AL035526) putative protein (fragment) [Arabidopsis thaliana]		UNCLASSIFIED	1024
4097	10173729 (8125, 8126)	Novel Protein sim. GBank gi 4539386 emb CAB37452.1 - (AL035526) extensin-like protein [Arabidopsis thaliana]		UNCLASSIFIED	1004

4098	78956879 (17899, 17900)	Novel Protein sim. GBank gil4539386 emb CAB37452.1 - (AL035526) exten:in-like protein [Arabidopsis thaliana]		UNCLASSIFIED	1054
4099	16329416 (18739, 18740)	Novel Protein sim. GBank gil4539386 emb CAB37452.1 - (AL035526) exten:in-like protein [Arabidopsis thaliana]		UNCLASSIFIED	1004
4100	47656627 (3953, 3954)	Novel Protein sim. GBank gil4539582 emb CAB38501.1 - (AL035636) putative sodium/proton antiporter [Streptomyces coelicolor]		UNCLASSIFIED	1029
4101	66694242 (5915, 5916)	Novel Protein sim. GBank gil4539582 emb CAB38501.1 - (AL035636) putative sodium/proton antiporter [Streptomyces coelicolor]		UNCLASSIFIED	1009
4102	20463731 (6383, 6384)	Novel Protein sim. GBank gil4545229 gb AAD22450.1 AF11618 - (AF11618) SecA homolog [Actinobacillus actinomycescomitans]		UNCLASSIFIED	1010
4103	9845416 (2423, 2424)	Novel Protein sim. GBank gil4545243 gb AAD22455.1 AF11628 - (AF116284) unknown [Pseudomonas aeruginosa]		UNCLASSIFIED	1023
4104	66051487 (8739, 8740)	Novel Protein sim. GBank gil4545243 gb AAD22455.1 AF11628 - (AF116284) unknown [Pseudomonas aeruginosa]		UNCLASSIFIED	1010
4105	9398483 (855, 856)	Novel Protein sim. GBank gil4567200 gb AAD23616.1 AC00716 - (AC007168) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	1017
4106	23332081 (18767, 18768)	Novel Protein sim. GBank gil4580470 gb AAD24394.1 AC00608 - (AC006081) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	1053

4107	80226635 (11291, 11292)	Novel Protein sim. GBank gi 4581504 emb CAB40163.1 - (AL049558) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	1006, 1010, 1024, 1027
4108	55004686 (751, 752)	Novel Protein sim. GBank gi 4583397 gb AAD25061.1 AF12100 - (AF121000) IS1628 transposase TrpB [Corynebacterium glutamicum]		UNCLASSIFIED	1019
4109	79605200 (9623, 9624)	Novel Protein sim. GBank gi 4583559 emb CAB40388.1 - (AJ005255) OxyR [Erwinia chrysanthemi]		UNCLASSIFIED	1034
4110	57147813 (14547, 14548)	Novel Protein sim. GBank gi 458420 (U06451) - proline permease homolog [Staphylococcus aureus]		UNCLASSIFIED	1004
4111	78916292 (5757, 5758)	Novel Protein sim. GBank gi 4584420 emb CAB40740.1 - (AJ011317) Orf361 [Aethylobacterium sp. CM4]		UNCLASSIFIED	1039
4112	79875001 (19585, 19586)	Novel Protein sim. GBank gi 4584438 emb CAB40701.1 - (AL049587) putative efflux protein [Streptomyces coelicolor]		UNCLASSIFIED	1017
4113	78764485 (14933, 14934)	Novel Protein sim. GBank gi 4584527 emb CAB40758.1 - (AL049607) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	1039
4114	79868279 (7851, 7852)	Novel Protein sim. GBank gi 4584539 emb CAB40769.1 - (AL049608) extensin-like protein [Arabidopsis thaliana]		UNCLASSIFIED	1025, 1031
4115	20177089 (19655, 19656)	Novel Protein sim. GBank gi 4585587 emb CAB40855.1 - (AL049628) putative adenine glycosylase [Streptomyces coelicolor]		UNCLASSIFIED	1010
4116	29912055 (6877, 6878)	Novel Protein sim. GBank gi 4586963 dbj BAA76556.1 - (AB018253) voltage- gated ca channel [Rattus norvegicus]		UNCLASSIFIED	1022
4117	11287498 (7595, 7596)	Novel Protein sim. GBank gi 4587313 dbj BAA76709.1 - (AB025248) alpha- 1,2-mannosidase [Bacillus sp. M-90]		UNCLASSIFIED	1022

4118	66727941 (18969, 18970)	Novel Protein sim. GBank gil4587326[dbj BAA76717.1] - (AB025424) aconitase [Corynebacterium glutamicum]		UNCLASSIFIED	1009
4119	78735337 (4713, 4714)	Novel Protein sim. GBank gil4587571[gb AAD25802.1 AC00655 - (AC006550) Belongs to the PFI01027 Uncharacterized protein family UPF0005 with 7 transmembrane domains. [Arabidopsis thaliana]		UNCLASSIFIED	1008
4120	8504857 (20305, 20306)	Novel Protein sim. GBank gil4588130[gb AAD25997.1 AF10254 - (AF102548) AT1 receptor-associated protein [Mus musculus]		UNCLASSIFIED	1024
4121	19869742 (12611, 12612)	Novel Protein sim. GBank gil4589366[gb AAD26468.1] - (AF140505) DEAD box RNA helicase [Candida albicans]		UNCLASSIFIED	1022
4122	79613010 (6539, 6540)	Novel Protein sim. GBank gil4583484[dbj BAA76770.1] - (AB023143) KIAAC926 protein [Homo sapiens]		UNCLASSIFIED	1025
4123	20729925 (12773, 12774)	Novel Protein sim. GBank gil4583636[dbj BAA76840.1] - (AB023213) KIAAC996 protein [Homo sapiens]		UNCLASSIFIED	1004
4124	20465916 (6553, 6554)	Novel Protein sim. GBank gil460249 (U07228) - Saccharomyces cerevisiae Rev7p (REV7) gene, complete cds. [Saccharomyces cerevisiae]		UNCLASSIFIED	1010, 1022
4125	80429246 (19267, 19268)	Novel Protein sim. GBank gil461402 (L29642) - methyltransferase [Pseudomonas fluorescens]		UNCLASSIFIED	1038
4126	79751472 (5807, 5808)	Novel Protein sim. GBank gil461623[sp P29853 BGAL_ASPNG - BETA- GALACTOSIDASE PRECURSOR (LACTASE)		UNCLASSIFIED	1003, 1004, 1009, 1054
4127	27962594 (9859, 9860)	Novel Protein sim. GBank gil461915[sp P33894 DAP1_YEAST - DIPEPTIDYL AMINOPEPTIDASE A (DPAP A) (YSCIV)		UNCLASSIFIED	1001, 1006, 1010, 1022, 1024, 1031, 1034

4128	19882613 (21315, 21316)	Novel Protein sim. GBank gi 462168 sp P33892 GCN1_YEAST - TRANSLATIONAL ACTIVATOR GCN1		UNCLASSIFIED	1022
4129	81918276 (7487, 7488)	Novel Protein sim. GBank gi 462569 sp P34926 MAPA_RAT - MICROTUBULE-ASSOCIATED PROTEIN 1A (CONTAINS: LIGHT CHAIN LC2)		UNCLASSIFIED	1054
4130	37809745 (11367, 11368)	Novel Protein sim. GBank gi 462569 sp P34926 MAPA_RAT - MICROTUBULE-ASSOCIATED PROTEIN 1A (CONTAINS: LIGHT CHAIN LC2)		UNCLASSIFIED	1058
4131	27851045 (22447, 22448)	Novel Protein sim. GBank gi 462623 sp Q00587 MSE5_HUMAN - SERUM PROTEIN MSE55		UNCLASSIFIED	1006, 1022
4132	80478201 (2967, 2968)	Novel Protein sim. GBank gi 462360 sp P33412 MUC1_YEAST - MUC1 PROTEIN		UNCLASSIFIED	1010, 1012, 1022, 1024
4133	16424704 (15095, 15096)	Novel Protein sim. GBank gi 463432 (U05214) - prolinase [Lactobacillus helveticus]		UNCLASSIFIED	1038
4134	78518093 (18819, 18820)	Novel Protein sim. GBank gi 4646206 gb AAD26879.1 AC00723 - (AC007230) Contains similarity to gb D13630 KIAA0005 gene from Homo sapiens. ESTs gb T45345, gb T21086, gb R90360, gb T20468, gb T45191 and gb A100459 come from this gene. [Arabiopsis thaliana]		UNCLASSIFIED	1017
4135	20463398 (6699, 6700)	Novel Protein sim. GBank gi 464758 sp P33330 SERC_YEAST - PHOSPHOSERINE AMINOTRANSFERASE (PSAT)		UNCLASSIFIED	1010, 1017
4136	80231895 (4801, 4802)	Novel Protein sim. GBank gi 464800 sp P34164 SIP2_YEAST - SIP2 PROTEIN (SPM2 PROTEIN)		UNCLASSIFIED	1008, 1022, 1024, 1025, 1026, 1031, 1038
4137	8368192 (75, 76)	Novel Protein sim. GBank gi 464826 sp P14825 SYK2_ECOLI - LYSYL- TRNA SYNTHETASE, HEAT INDUCIBLE (LYSINE--TRNA LIGASE) (LYSRS)		UNCLASSIFIED	1022

4138	79830712 (17289, 17290)	Novel Protein sim. GBank gil4678137 emb CAB41210.1 - (AL049661) putative lipoprotein [Streptomyces coelicolor]		UNCLASSIFIED	1039
4139	85800726 (14201, 14202)	Novel Protein sim. GBank gil4678899 emb CAB41271.1 - (AL049707) putative large glycine/alanine rich protein [Streptomyces coelicolor]		UNCLASSIFIED	1025
4140	78891820 (8907, 8908)	Novel Protein sim. GBank gil4680645 gb AAD27712.1 AF13293 - (AF132937) CGI-02 protein [Homo sapiens]		UNCLASSIFIED	1006, 1038
4141	30259427 (22745, 22746)	Novel Protein sim. GBank gil4680645 gb AAD27712.1 AF13293 - (AF132937) CGI-02 protein [Homo sapiens]		UNCLASSIFIED	1008
4142	79844531 (21555, 21556)	Novel Protein sim. GBank gil4680671 gb AAD27725.1 AF13295 - (AF132950) CGI-16 protein [Homo sapiens]		UNCLASSIFIED	1008
4143	56152827 (20579, 20580)	Novel Protein sim. GBank gil4691726 gb AAD28046.1 AF12449 - (AF124490) ARF GTPase-activating protein GIT1 [Homo sapiens]		UNCLASSIFIED	1003
4144	28387803 (15615, 15616)	Novel Protein sim. GBank gil4725999 emb CAB41728.1 - (AL049731) putative transpeptidase [Streptomyces coelicolor]		UNCLASSIFIED	1016
4145	85528995 (479, 480)	Novel Protein sim. GBank gil4753853 emb CAB42016.1 - (AL049754) putative adenylosuccinate synthetase [Streptomyces coelicolor]		UNCLASSIFIED	1049
4146	20437227 (13685, 13686)	Novel Protein sim. GBank gil4753871 emb CAB42034.1 - (AL049754) hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	1010
4147	16327929 (9021, 9022)	Novel Protein sim. GBank gil4757095 emb CAB42080.1 - (AL049763) conserved hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	1004

4148	94324296 (13171, 13172)	Novel protein sim. GBank gi 4757846 ref NP_004317.1 pBCL9 - B-cell CLL lymphoma 9		UNCLASSIFIED	1044
4149	58214305 (12441, 12442)	Novel Protein sim. GBank gi 4753028 ref NP_004361.1 pCOL1 - collagen, type XI, alpha 1		UNCLASSIFIED	1038
4150	81652285 (5527, 5528)	Novel Protein sim. GBank gi 4761595 gb AAD29417.1 AF13195 - (AF131951) Shank1a [Rattus norvegicus]		UNCLASSIFIED	1010, 1054
4151	10253081 (4243, 4244)	Novel Protein sim. GBank gi 476794 pir A40678 - T-cell adhesion receptor CD2 homolog - African swine fever virus		UNCLASSIFIED	1038
4152	80200962 (8715, 8716)	Novel Protein sim. GBank gi 4768831 gb AAD29633.1 AF11682 - (AF113827) unknown [Homo sapiens]		UNCLASSIFIED	1022, 1034
4153	20724136 (11269, 11270)	Novel Protein sim. GBank gi 4763871 gb AAD29665.1 AF12475 - (AF124757) acetohydroxy acid isomeroreductase [Zymomonas mobilis]		UNCLASSIFIED	1006
4154	65460060 (1823, 1824)	Novel Protein sim. GBank gi 477140 pir A48151 - sperm tail protein Mst98Ca - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	1054
4155	11392439 (4437, 4438)	Novel Protein sim. GBank gi 4773908 gb AAD29778.1 AF14725 - (AF147259) No definition line found [Arabidopsis thaliana]		UNCLASSIFIED	1024
4156	27965858 (5467, 5468)	Novel Protein sim. GBank gi 478426 pir JX0282 - sensory kinase BaeS protein - Escherichia coli		UNCLASSIFIED	1006
4157	80221143 (4291, 4292)	Novel Protein sim. GBank gi 479628 pir S34969 - porin E1 - Pseudomonas aeruginosa		UNCLASSIFIED	1024
4158	79181138 (16065, 16066)	Novel Protein sim. GBank gi 479628 pir S34969 - porin E1 - Pseudomonas aeruginosa		UNCLASSIFIED	1022

4159	8756873 (17653, 17654)	Novel Protein sim. GBank gij48057Q pir S37051 - 4-hydroxybenzoate 3-monooxygenase (EC 1.14.13.2) - <i>Pseudomonas</i> sp	UNCLASSIFIED	1004
4160	57308551 (20083, 20084)	Novel Protein sim. GBank gij4808335 emb CAB42749.1 - (AL049841) putative membrane protein [Streptomyces coelicolor]	UNCLASSIFIED	1024
4161	20710329 (3021, 3022)	Novel Protein sim. GBank gij4808345 emb CAB42759.1 - (AL049841) hypothetical protein [Streptomyces coelicolor]	UNCLASSIFIED	1006
4162	20465744 (19597, 19598)	Novel Protein sim. GBank gij4808350 emb CAB42764.1 - (AL049841) possible membrane protein [Streptomyces coelicolor]	UNCLASSIFIED	1010
4163	10872434 (14867, 14868)	Novel Protein sim. GBank gij4808397 emb CAB42729.1 - (AL049826) putative penicillin-binding protein [Streptomyces coelicolor]	UNCLASSIFIED	1004
4164	66729137 (16609, 16610)	Novel Protein sim. GBank gij4808398 emb CAB42730.1 - (AL049826) putative transmembrane protein [Streptomyces coelicolor]	UNCLASSIFIED	1049
4165	79264999 (10189, 10190)	Novel Protein sim. GBank gij481728 pir S39206 - hypothetical protein 1 - rat	UNCLASSIFIED	1007
4166	6749280 (9719, 9720)	Novel Protein sim. GBank gij4826521 emb CAB42853.1 - (AL035402) dJ88J8.1 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like protein) (hs6M1-15)) [Homo sapiens]	UNCLASSIFIED	1022
4167	54680542 (1323, 1324)	Novel Protein sim. GBank gij4826816 ref NP_005088.1 pLG11 - leucine-rich, glioma inactivated 1	UNCLASSIFIED	1040, 1041, 1042
4168	55393532 (10683, 10684)	Novel Protein sim. GBank gij4826914 ref NP_005081.1 pPLA2 - phospholipase A2, group IVB (cytosolic)	UNCLASSIFIED	1000

4169	30522889 (16177, 16178)	Novel Protein sim. GBank gil4826934 ref NP_005125.1 pPPP4 - protein phosphatase 4, regulatory subunit 1		UNCLASSIFIED	1009
4170	79177363 (13127, 13128)	Novel Protein sim. GBank gil4826998 ref NP_005057.1 pSFPQ - splicing factor proline/glutamine rich (polypyrimidine tract- binding protein-associated)		UNCLASSIFIED	1024
4171	20289541 (15699, 15700)	Novel Protein sim. GBank gil4836574 gb AAD30493.1 AF12644 - (AF126447) tryptophan monooxygenase [Agrobacterium vitis]		UNCLASSIFIED	1034
4172	20182178 (15287, 15288)	Novel Protein sim. GBank gil4836930 gb AAD30632.1 AC00608 - (AC006085) Hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	1024
4173	20480441 (5001, 5002)	Novel Protein sim. GBank gil484643 pir JQ2260 - proline-rich cell wall protein - carrot		UNCLASSIFIED	1022
4174	20480205 (22809, 22810)	Novel Protein sim. GBank gil484643 pir JQ2260 - proline-rich cell wall protein - carrot		UNCLASSIFIED	1034
4175	47656561 (17535, 17536)	Novel Protein sim. GBank gil4850259 emb CAB43030.1 - (AJ239085) hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	1029, 1053
4176	54817126 (2723, 2724)	Novel Protein sim. GBank gil488342 dbj BAA05089 - (D26094) 6- aminohexanoate-dimer hydrolase [Flavobacterium sp.]		UNCLASSIFIED	1029
4177	79470584 (22685, 22686)	Novel Protein sim. GBank gil4883446 emb CAB43156.1 - (AL049913) hypothetical protein MLCB1610.10 [Mycobacterium leprae]		UNCLASSIFIED	1022
4178	95009100 (20151, 20152)	Novel Protein sim. GBank gil4884836 gb AAD31829.1 - (AF131877) NapG oxidoreductase [Streptomyces collinus]		UNCLASSIFIED	1017

4179	78512479 (18051, 18052)	Novel Protein sim. GBank gi 4885183 ref NP_005210.1 pDIAP - diaphanous (Drosophila, homolog) 1		UNCLASSIFIED	1026
4180	77516883 (189, 190)	Novel Protein sim. GBank gi 4887208 gb AAD32235.1 AF14744 - (AF147448) unknown [Pseudomonas aeruginosa]		UNCLASSIFIED	1049
4181	20729752 (11095, 11096)	Novel Protein sim. GBank gi 4887209 gb AAD32236.1 AF14744 - (AF147448) lipote biosynthesis protein B [Pseudomonas aeruginosa]		UNCLASSIFIED	1006, 1010, 1022
4182	28842901 (20739, 20740)	Novel Protein sim. GBank gi 4887715 gb AAA79329.2 - (L08811) adherin [Drosophila melanogaster]		UNCLASSIFIED	1008
4183	78790738 (7147, 7148)	Novel Protein sim. GBank gi 4895190 gb AAD32777.1 AC00766 - (AC007661) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	1026
4184	17876820 (15297, 15298)	Novel Protein sim. GBank gi 4902474 emb CAB43554.1 - (AJ131243) 5'- nucleotidase [Columba livia]		UNCLASSIFIED	1024
4185	70336498 (13655, 13656)	Novel Protein sim. GBank gi 4928283 gb AAD33519.1 AF13212 - (AF132127) sorbitol operon regulator [Streptococcus mutans]		UNCLASSIFIED	1049
4186	29676495 (8163, 8164)	Novel Protein sim. GBank gi 4928699 gb AAD33689.1 AF13640 - (AF136403) unknown [Pseudomonas aeruginosa]		UNCLASSIFIED	1054
4187	10183752 (1911, 1912)	Novel Protein sim. GBank gi 496100 (L24560) - unknown function; putative [Bacteriophage phi- LC3]		UNCLASSIFIED	1003
4188	17300825 (9581, 9582)	Novel Protein sim. GBank gi 4972692 gb AAD34741.1 - (AF132153) unknown [Drosophila melanogaster]		UNCLASSIFIED	1008

4189	86692752 (18605, 18606)	Novel Protein sim. GBank gil4980555[gb]/AAD35162.1 AE00169 - (AE001693) D-mannanase oxidoreductase, putative [Thermotoga maritima]		UNCLASSIFIED	1018, 1029
4190	46797503 (12589, 12590)	Novel Protein sim. GBank gil4980744[gb]/AAD35336.1 AE00170 - (AE001708) Na-translocating NADH-quinone reductase, Nqr2 subunit [Thermotoga maritima]		UNCLASSIFIED	1029
4191	20628084 (15171, 15172)	Novel Protein sim. GBank gil4981025[gb]/AAD35598.1 AE00172 - (AE001727) comM protein [Thermotoga maritima]		UNCLASSIFIED	1010
4192	20627760 (8073, 8074)	Novel Protein sim. GBank gil4981496[gb]/AAD36037.1 AE00175 - (AE001759) ribose ABC transporter, periplasmic ribose-binding protein [Thermotoga maritima]		UNCLASSIFIED	1010
4193	37800159 (8367, 8368)	Novel Protein sim. GBank gil4981511[gb]/AAD36051.1 AE00176 - (AE001760) conserved hypothetical protein, GGDEF domain [Thermotoga maritima]		UNCLASSIFIED	1012
4194	20696482 (6973, 6974)	Novel Protein sim. GBank gil4982168[gb]/AAD36664.1 AE00180 - (AE001804) hypothetical protein [Thermotoga maritima]		UNCLASSIFIED	1004
4195	80505265 (6509, 6510)	Novel Protein sim. GBank gil4982300[gb]/AAD36789.1 AE00181 - (AE001811) conserved hypothetical protein [Thermotoga maritima]		UNCLASSIFIED	1012
4196	18536655 (2553, 2554)	Novel Protein sim. GBank gil4995988[dbj]/BAA78221.1 - (AB021506) 25.6% identical to U1 gene of strain U1102 of HHV-6 [Human herpesvirus 6]		UNCLASSIFIED	1017
4197	94723956 (9067, 9068)	Novel Protein sim. GBank gil4996126[dbj]/BAA78341.1 - (AB017551) 16G2 [Homo sapiens]		UNCLASSIFIED	1004, 1010, 1034

4198	78379623 (3355, 3356)	Novel Protein sim. GBank gil5002553[gb]/AAD37457.1] - (AF074603) NonF [Streptomyces griseus subsp. griseus]		UNCLASSIFIED	1008
4199	11306440 (9019, 9020)	Novel Protein sim. GBank gil5002556[gb]/AAD37460.1] - (AF074603) putative flavoprotein reductase; NonH [Streptomyces griseus subsp. griseus]		UNCLASSIFIED	1010
4200	77473409 (2891, 2892)	Novel Protein sim. GBank gil5006424[gb]/AAD37493.1 AF10916 - (AF109162) HmuT precursor [Corynebacterium diphtheriae]		UNCLASSIFIED	1023
4201	23291965 (2719, 2720)	Novel Protein sim. GBank gil5019326[emb]/CAB44379.1] - (AL078610) putative integral membrane protein [Streptomyces coelicolor]		UNCLASSIFIED	1017
4202	46571483 (22719, 22720)	Novel Protein sim. GBank gil5019350[emb]/CAB44403.1] - (AL078610) putative heavy metal reductase [Streptomyces coelicolor]		UNCLASSIFIED	1029
4203	20478425 (6781, 6782)	Novel Protein sim. GBank gil5031649[ref]/NP_005791.1 pD13S - highly charged protein		UNCLASSIFIED	1022
4204	11198755 (15589, 15590)	Novel Protein sim. GBank gil5031657[ref]/NP_005755.1 pDD96 - epithelial protein up-regulated in carcinoma		UNCLASSIFIED	1004
4205	78259691 (20061, 20062)	Novel Protein sim. GBank gil5031889[ref]/NP_005570.1 pLRE1 - LINE retrotransposable element 1		UNCLASSIFIED	1026
4206	82296248 (21617, 21618)	Novel Protein sim. GBank gil5042237[emb]/CAB44655.1] - (Y18605) hypothetical protein RvD1-Rv2024c [Mycobacterium bovis BCG]		UNCLASSIFIED	1001, 1017, 1038
4207	37802702 (21535, 21536)	Novel Protein sim. GBank gil5051775[emb]/CAB45068.1] - (AL078637) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	1058

4208	29026177 (13021, 13022)	Novel Protein sim. GBank gil5069461 gb AAD39017.1 - (AF026270) PduS [Salmonella enterica serovar Typhimurium]		UNCLASSIFIED	1017
4209	11100488 (6163, 6164)	Novel Protein sim. GBank gil5091481 gb AAD39554.1 - (AF031417) TtgC [Pseudomonas putida]		UNCLASSIFIED	1022
4210	78891509 (18777, 18778)	Novel Protein sim. GBank gil5102805 emb CAB45220.1 - (AL079308) putative membrane protein [Streptomyces coelicolor]		UNCLASSIFIED	1017, 1026
4211	78794320 (15629, 15630)	Novel Protein sim. GBank gil5103837 gb AAD39667.1 AC00759 - (AC007591) Simalar to gil4377403 Polypeptide Deformylase from Chlamydia pneumoniae genome gb AE001687. [Arabidopsis thaliana]		UNCLASSIFIED	1026
4212	38327895 (2463, 2464)	Novel Protein sim. GBank gil5103846 gb AAD39676.1 AC00759 - (AC007591) F9L1.43 [Arabidopsis thaliana]		UNCLASSIFIED	1008
4213	9849193 (13849, 13650)	Novel Protein sim. GBank gil5104588 db BAA79903.1 - (AP000060) 254aa long hypothetical high-affinity branched-chain amino acid transport ATP-binding protein [Aeropyrum pernix]		UNCLASSIFIED	1008
4214	19867362 (10401, 10402)	Novel Protein sim. GBank gil5105618 db BAA80931.1 - (AP000062) 121aa long hypothetical protein [Aeropyrum pernix]		UNCLASSIFIED	1001
4215	65453050 (17801, 17802)	Novel Protein sim. GBank gil5107805 gb AAD25110.2 AF14055 - (AF140550) ShdA [Salmonella typhimurium]		UNCLASSIFIED	1049
4216	79951990 (18955, 18956)	Novel Protein sim. GBank gil5114184 gb AAD40230.1 AF12349 - (AF123492) Era [Pseudomonas aeruginosa]		UNCLASSIFIED	1001
4217	17882402 (1919, 1920)	Novel Protein sim. GBank gil5123651 emb CAB45340.1 - (AL079345) putative aminotransferase [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	1039

4218	33202398 (7315, 7316)	Novel Protein sim. GBank gil5123878[emb]CAB45470.1 - (AL079348) putative Na(+)/H(+) antiporter [Streptomyces coelicolor]		UNCLASSIFIED	1026
4219	78361326 (9315, 9316)	Novel Protein sim. GBank gil5123926[emb]CAB45514.1 - (AL079350) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	1003, 1044
4220	86474002 (14447, 14448)	Novel Protein sim. GBank gil5123944[emb]CAB45502.1 - (AL079349) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	1054
4221	78484644 (20047, 20048)	Novel Protein sim. GBank gil5139569[emb]CAB45587.1 - (AL079355) putative transcriptional regulator [Streptomyces coelicolor]		UNCLASSIFIED	1008
4222	34892544 (10233, 10234)	Novel Protein sim. GBank gil5139585[emb]CAB45603.1 - (AL079356) polyketide hydroxylase [Streptomyces coelicolor]		UNCLASSIFIED	1050
4223	80471534 (5325, 5326)	Novel Protein sim. GBank gil5139634[emb]CAB45563.1 - (AL079353) putative penicillin-binding protein [Streptomyces coelicolor]		UNCLASSIFIED	1012, 1024, 1027, 1031
4224	80501776 (14517, 14518)	Novel Protein sim. GBank gil515507 (U12027) - Sok1p [Saccharomyces cerevisiae]		UNCLASSIFIED	1003, 1004, 1009, 1012, 1022
4225	94991800 (3069, 3070)	Novel Protein sim. GBank gil516764[dbj]BAA04654 - (D21092) motor protein [Homo sapiens]		UNCLASSIFIED	1022
4226	30259581 (18109, 18110)	Novel Protein sim. GBank gil5174723[ref]NP_006105.1 pTOM4 - mitochondrial outer membrane protein		UNCLASSIFIED	1008
4227	78405088 (613, 614)	Novel Protein sim. GBank gil5257110[dbj]BAA81784.1 - (AB011418) orf5 [Alteromonas sp. B-10-31]		UNCLASSIFIED	1024
4228	16456835 (13059, 13060)	Novel Protein sim. GBank gil5262762[emb]CAB45910.1 - (AL080283) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	1008

4229	79115440 (17561, 17562)	Novel Protein sim. GBank gi 5262775 emb CAB45880.1 - (AL080282) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	1003
4230	25261625 (11719, 11720)	Novel Protein sim. GBank gi 5305335 gb AAD41594.1 AF07108 - (AF071081) proline-rich mucin homolog [Mycobacterium tuberculosis]		UNCLASSIFIED	1008
4231	21637022 (20197, 20198)	Novel Protein sim. GBank gi 5306245 gb AAD41878.1 AC00643 - (AC006438) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	1017, 1038
4232	29024921 (19337, 19338)	Novel Protein sim. GBank gi 532549 (U09422) - ORF16 [Enterococcus faecalis]		UNCLASSIFIED	1017
4233	30256223 (21613, 21614)	Novel Protein sim. GBank gi 5354158 gb AAD42378.1 AF14984 - (AF149841) digalactosyl diacylglycerol synthase [Arabidopsis thaliana]		UNCLASSIFIED	1024
4234	10107781 (22951, 22952)	Novel Protein sim. GBank gi 5354198 gb AAD42407.1 AF15749 - (AF157493) hypothetical protein [Zymomonas mobilis]		UNCLASSIFIED	1017
4235	28848542 (18401, 18402)	Novel Protein sim. GBank gi 538683 pir A42800 - beta-alanine--pyruvate transaminase (EC 2.6.1.18) - Pseudomonas putida		UNCLASSIFIED	1026
4236	28477465 (14763, 14764)	Novel Protein sim. GBank gi 539030 pir B48232 - cysteine-rich extensin-like protein 2 precursor - common tobacco		UNCLASSIFIED	1008
4237	29272904 (20963, 20964)	Novel Protein sim. GBank gi 539244 pir S38100 - hypothetical protein YKR028w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1022
4238	80218605 (9611, 9612)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	1001, 1004, 1006, 1008, 1009, 1010, 1016, 1022, 1024, 1026, 1029, 1034

4239	20292803 (9911, 9912)	Novel Protein sim. GBank gil5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	1034
4240	20451411 (16493, 16494)	Novel Protein sim. GBank gil5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	1024
4241	70504276 (3179, 3180)	Novel Protein sim. GBank gil5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	1019, 1036
4242	20608432 (3971, 3972)	Novel Protein sim. GBank gil5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	1004
4243	79619222 (5367, 5368)	Novel Protein sim. GBank gil5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	1038
4244	47660024 (17439, 17440)	Novel Protein sim. GBank gil5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	1029
4245	70942086 (21949, 21950)	Novel Protein sim. GBank gil5430769 gb AAD43169.1 AC00750 - (AC007504) Similar to somatic embryogenesis receptor-like kinase [Arabidopsis thaliana]	UNCLASSIFIED	1024
4246	19541721 (5161, 5162)	Novel Protein sim. GBank gil543415 pir PC2022 - mucin like protein Muc2 precursor - rat (fragment)	UNCLASSIFIED	1004
4247	79819430 (22981, 22982)	Novel Protein sim. GBank gil543804 sp P36670 AMPG_ECOLI - AMPG PROTEIN	UNCLASSIFIED	1001
4248	79771201 (5399, 5400)	Novel Protein sim. GBank gil544119 sp Q05766 CYAA_PASMU - ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE) (ADENYLATE CYCLASE)	UNCLASSIFIED	1034
4249	27844539 (3055, 3056)	Novel Protein sim. GBank gil544346 sp Q05860 FORM_MOUSE - FORMIN (LIMB DEFORMITY PROTEIN)	UNCLASSIFIED	1006

4250	78154058 (11841, 11842)	Novel Protein sim. GBank gi 544348 sp Q05860 FORM_MOUSE - FORMIN (LIMB DEFECT FORMITY PROTEIN)		UNCLASSIFIED	1030, 1050
4251	78369003 (16773, 16774)	Novel Protein sim. GBank gi 544374 sp P36417 GBF_DICD1 - G-BOX BINDING FACTOR (GBF)		UNCLASSIFIED	1008
4252	20385892 (13713, 13714)	Novel Protein sim. GBank gi 5457261 emb CAB46949.1 - (AL096822) putative membrane protein [Streptomyces coelicolor]		UNCLASSIFIED	1004
4253	21426446 (20105, 20106)	Novel Protein sim. GBank gi 5457287 emb CAB46974.1 - (AL096825) hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	1006
4254	30786324 (10973, 10974)	Novel Protein sim. GBank gi 5457403 emb CAB48401.1 - (AJ238332) death inducer-3bilitator-1 [Mus musculus]		UNCLASSIFIED	1009
4255	79199218 (15631, 15632)	Novel Protein sim. GBank gi 5457574 emb CAB49065.1 - (AJ248283) PAB0091 [Pyrococcus abyss]		UNCLASSIFIED	1006, 1024
4256	20370177 (11947, 11948)	Novel Protein sim. GBank gi 5457720 emb CAB49211.1 - (AJ248283) hypothetical protein [Pyrococcus abyss]		UNCLASSIFIED	1004, 1006, 1010
4257	27787812 (215, 216)	Novel Protein sim. GBank gi 5457887 emb CAB49377.1 - (AJ248284) PAB0305 [Pyrococcus abyss]		UNCLASSIFIED	1034
4258	10173969 (14291, 14292)	Novel Protein sim. GBank gi 5458864 emb CAB50351.1 - (AJ248287) PAB2374 [Pyrococcus abyss]		UNCLASSIFIED	1023
4259	88094448 (4443, 4444)	Novel Protein sim. GBank gi 5459219 emb CAB48892.1 - (AL096837) hypothetical protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	1006
4260	86465171 (703, 704)	Novel Protein sim. GBank gi 5459220 emb CAB48893.1 - (AL096837) putative iron-sulfur protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	1029

4261	20466319 (863, 864)	Novel Protein sim. GBank gil5459220 emb CAB48893.1 - (AL096837) putative iron-sulfur protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	1010
4262	29357646 (11391, 11392)	Novel Protein sim. GBank gil5459220 emb CAB48893.1 - (AL096837) putative iron-sulfur protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	1008
4263	35896045 (15247, 15248)	Novel Protein sim. GBank gil5459392 emb CAB50750.1 - (AL096839) conserved hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	1053
4264	88094861 (20165, 20166)	Novel Protein sim. GBank gil5459401 emb CAB50759.1 - (AL096839) putative cytochrome oxidase assembly factor [Streptomyces coelicolor]		UNCLASSIFIED	1004, 1010, 1022
4265	21129728 (19259, 19260)	Novel Protein sim. GBank gil547653 sp P35915 HMGL_CHICK - HYDROXYMETHYLGLUTARYL-COA LYASE (HMG-COA LYASE) (HL) (3-HYDROXY-3- METHYLGLUTARATE-COA LYASE)		UNCLASSIFIED	1034
4266	25267091 (13835, 13836)	Novel Protein sim. GBank gil5478797 dbj BAA82479.1 - (AB021310) chlorophyll b synthase [Oryza sativa]		UNCLASSIFIED	1023
4267	65661339 (17341, 17342)	Novel Protein sim. GBank gil5485664 sp P36304 POLR_KYMVJ - RNA REPLICASE POLYPROTEIN		UNCLASSIFIED	1016
4268	78761774 (13415, 13416)	Novel Protein sim. GBank gil548582 sp P10963 PPCK_YEAST - PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP)		UNCLASSIFIED	1044
4269	80409035 (6347, 6348)	Novel Protein sim. GBank gil548705 sp P36949 RBSB_BACSU - D-RIBOSE- BINDING PROTEIN PRECURSOR		UNCLASSIFIED	1029

4270	8523867 (18799, 18800)	Novel Protein sim. GBank gil548925 sp P36024 SIS2_YEAST - SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3)		UNCLASSIFIED	1022
4271	65894777 (11929, 11930)	Novel Protein sim. GBank gil549613 sp P36136 YK23_YEAST - HYPOTHETICAL 31.0 KD PROTEIN IN GAP1- NAP1 INTERGENIC REGION		UNCLASSIFIED	1016, 1023
4272	28486888 (5997, 5998)	Novel Protein sim. GBank gil549624 sp P36146 LAS1_YEAST - LAS1 PROTEIN		UNCLASSIFIED	1026
4273	85513339 (15099, 15100)	Novel Protein sim. GBank gil549634 sp P36156 YK56_YEAST - HYPOTHETICAL 43.3 KD PROTEIN IN SIS2- MTD1 INTERGENIC REGION		UNCLASSIFIED	1001, 1003, 1006, 1008, 1009, 1010, 1012, 1016, 1017, 1022, 1023, 1024, 1025, 1026, 1027, 1031, 1034, 1038, 1039, 1044, 1049
4274	29261145 (11205, 11206)	Novel Protein sim. GBank gil549636 sp P36158 YK58_YEAST - HYPOTHETICAL 68.3 KD PROTEIN IN SIS2- MTD1 INTERGENIC REGION		UNCLASSIFIED	1009
4275	25341189 (7617, 7618)	Novel Protein sim. GBank gil549643 sp P36165 YK69_YEAST - HYPOTHETICAL 102.7 KD PROTEIN IN PRP16- SRP40 INTERGENIC REGION		UNCLASSIFIED	1044
4276	78461719 (13971, 13972)	Novel Protein sim. GBank gil549643 sp P36165 YK69_YEAST - HYPOTHETICAL 102.7 KD PROTEIN IN PRP16- SRP40 INTERGENIC REGION		UNCLASSIFIED	1008
4277	80027280 (6545, 6546)	Novel Protein sim. GBank gil549704 sp P36075 YKJ0_YEAST - HYPOTHETICAL 50.9 KD PROTEIN IN BUD2- MIF2 INTERGENIC REGION		UNCLASSIFIED	1001, 1004, 1006

4278	20484209 (13947, 13948)	Novel Protein sim. GBank gi 549734 sp P36051 YKQ5 YEAST - HYPOTHETICAL 105.7 KD PROTEIN IN TPK3- PIR1 INTERGENIC REGION		UNCLASSIFIED	1010
4279	80217125 (6487, 6488)	Novel Protein sim. GBank gi 549767 sp P36111 YKZ5 YEAST - HYPOTHETICAL 66.6 KD PROTEIN IN YPT52- DBP7 INTERGENIC REGION		UNCLASSIFIED	1004, 1008, 1009, 1022, 1024, 1029
4280	79615128 (7139, 7140)	Novel Protein sim. GBank gi 549814 sp Q01856 YRDX_RHOSH - HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN RDXA 3'REGION		UNCLASSIFIED	1003
4281	78245861 (3899, 3900)	Novel Protein sim. GBank gi 549854 (U07615) - mucin [Rattus norvegicus]		UNCLASSIFIED	1006
4282	32275610 (579, 580)	Novel Protein sim. GBank gi 5514778 emb CAB50780.1 - (X74218) Tola protein [Pseudomonas putida]		UNCLASSIFIED	1029
4283	25263625 (3835, 3836)	Novel Protein sim. GBank gi 5514781 emb CAB50783.1 - (X74218) hypothetical protein [Pseudomonas putida]		UNCLASSIFIED	1026
4284	37797702 (12461, 12462)	Novel Protein sim. GBank gi 5525064 emb CAB50880.1 - (AL096844) putative integral membrane transporter [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	1012
4285	80502199 (12497, 12498)	Novel Protein sim. GBank gi 5531366 emb CAB50998.1 - (AL096852) hypothetical protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	1003, 1008, 1010, 1012, 1024
4286	86471967 (9293, 9294)	Novel Protein sim. GBank gi 5531906 gb AAD44524.1 AF10740 - (AF107406) GW128 [Homo sapiens]		UNCLASSIFIED	1029
4287	80227840 (13667, 13668)	Novel Protein sim. GBank gi 554015 (M37679) - Ig heavy chain precursor [Mus musculus]		UNCLASSIFIED	1006
4288	47657338 (1277, 1278)	Novel Protein sim. GBank gi 556614 (U14909) - MtrB [Mycobacterium tuberculosis]		UNCLASSIFIED	1029

4289	80503062 (15163, 15164)	Novel Protein sim. GBank gil5578872 emb CAB51274.1 - (AL096872) hypothetical protein [Streptomyces coelicolor A3(2)]	UNCLASSIFIED	1004, 1006, 1012, 1017, 1024, 1034
4290	80248867 (16467, 16468)	Novel Protein sim. GBank gil5578875 emb CAB51277.1 - (AL096872) putative lipote-protein ligase [Streptomyces coelicolor A3(2)]	UNCLASSIFIED	1006, 1053
4291	79319416 (2413, 2414)	Novel Protein sim. GBank gil5579421 gb AAD45542.1 U70376_ - (U70376) Orf2 [Streptomyces flavopersicus]	UNCLASSIFIED	1022
4292	27977871 (1525, 1526)	Novel Protein sim. GBank gil5596803 emb CAB51450.1 - (AL096884) putative transcriptional regulatory protein [Streptomyces coelicolor A3(2)]	UNCLASSIFIED	1006
4293	27366056 (9249, 9250)	Novel Protein sim. GBank gil5613074 gb AAD45616.1 AF06194 - (AF06194) protate-derived STE20-like kinase PSK [Homo sapiens]	UNCLASSIFIED	1022
4294	24144612 (15437, 15438)	Novel Protein sim. GBank gil5640135 emb CAA64209.1 - (X94435) ribosomal protein TL5 [Thermus thermophilus]	UNCLASSIFIED	1001, 1003
4295	27956094 (22021, 22022)	Novel Protein sim. GBank gil5668580 gb AAD45964.1 AF05115 - (AF05115) aspartyl protease [Mus musculus]	UNCLASSIFIED	1004, 1022
4296	28474907 (20215, 20216)	Novel Protein sim. GBank gil5668806 gb AAD46032.1 AC00751 - (AC00751) Strong similarity to F16N3.17 from Arabidopsis thalian BAC gb AC007519. [Arabidopsis thaliana]	UNCLASSIFIED	1026
4297	94631802 (4247, 4248)	Novel Protein sim. GBank gil5688851 dbj BAA82702.1 - (AB017438) Orf5 [Streptomyces coelicolor]	UNCLASSIFIED	1006, 1031
4298	10083399 (1191, 1192)	Novel Protein sim. GBank gil5689395 dbj BAA82981.1 - (AB028952) KIAA1029 protein [Homo sapiens]	UNCLASSIFIED	1044

4299	78936219 (17531, 17532)	Novel Protein sim. GBank gil56894t5dbj BAA83016.1 - (AB028987) KIAA1051 protein [Homo sapiens]	UNCLASSIFIED	1044, 1050
4300	13088718 (18587, 18588)	Novel Protein sim. GBank gil56894t5dbj BAA83029.1 - (AB029000) KIAA1071 protein [Homo sapiens]	UNCLASSIFIED	1027
4301	24121020 (10605, 10606)	Novel Protein sim. GBank gil56895t3dbj BAA83040.1 - (AB029011) KIAA1088 protein [Homo sapiens]	UNCLASSIFIED	1029
4302	88095233 (17405, 17406)	Novel Protein sim. GBank gil56895t5dbj BAA83046.1 - (AB029017) KIAA1094 protein [Homo sapiens]	UNCLASSIFIED	1034
4303	30660456 (4139, 4140)	Novel Protein sim. GBank gil56895t1dbj BAA83059.1 - (AB029030) KIAA1101 protein [Homo sapiens]	UNCLASSIFIED	1026
4304	30660312 (9653, 9654)	Novel Protein sim. GBank gil56895t1dbj BAA83059.1 - (AB029030) KIAA1101 protein [Homo sapiens]	UNCLASSIFIED	1026
4305	78459851 (8605, 8606)	Novel Protein sim. GBank gil56898t3emb CAB52046.1 - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)]	UNCLASSIFIED	1023, 1026, 1029, 1053
4306	20286969 (17575, 17576)	Novel Protein sim. GBank gil56899t5emb CAB51995.1 - (AL109663) putative UDP-N-acetylmutaromylalanine-D-glutamate ligase [Streptomyces coelicolor A3(2)]	UNCLASSIFIED	1004, 1006, 1025, 1034
4307	79822009 (16001, 16002)	Novel Protein sim. GBank gil56899t6emb CAB51998.1 - (AL109663) putative UDP-N-acetylmutaromylalanine-D-glutamate-2,6-diaminopimelate ligase [Streptomyces coelicolor A3(2)]	UNCLASSIFIED	1034
4308	79631297 (8077, 8078)	Novel Protein sim. GBank gil56899t7emb CAB52004.1 - (AL109663) putative membrane protein [Streptomyces coelicolor A3(2)]	UNCLASSIFIED	1006, 1023, 1027

4309	11085397 (19439, 19440)	Novel Protein sim. GBank gi 5690013 emb CAB51940.1 - (AJ132472) Putative ABC-type Sugar Transporter [Ruminococcus flavefaciens]		UNCLASSIFIED	1024
4310	13418034 (21103, 21104)	Novel Protein sim. GBank gi 5708250 emb CAB52363.1 - (AL109747) putative integral membrane protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	1022
4311	11817576 (17589, 17590)	Novel Protein sim. GBank gi 584706 sp P37833 AATC_ORYSA - ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)		UNCLASSIFIED	1004
4312	78895482 (22707, 22708)	Novel Protein sim. GBank gi 585369 sp P38620 KPR2_YEAST - RIBOSE- PHOSPHATE PYROPHOSPHOKINASE 2 (PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 2)		UNCLASSIFIED	1039
4313	11611991 (7747, 7748)	Novel Protein sim. GBank gi 585377 sp P38131 KTR4_YEAST - PROBABLE MANNOSYLTRANSFERASE KTR4		UNCLASSIFIED	1006
4314	80237342 (17327, 17328)	Novel Protein sim. GBank gi 585465 sp P29469 MCM2_YEAST - MINICHROMOSOME MAINTENANCE PROTEIN 2		UNCLASSIFIED	1006, 1008, 1009, 1022, 1034
4315	13523408 (21665, 21666)	Novel Protein sim. GBank gi 585774 sp P24386 RAE1_HUMAN - RAB PROTEINS GERANYLGERANYLTRANSFERASE COMPONENT A 1 (RAB ESCORT PROTEIN 1) (REP-1) (CHOROIDEAEMIA PROTEIN) (TCD PROTEIN)		UNCLASSIFIED	1024
4316	79763698 (14811, 14812)	Novel Protein sim. GBank gi 586056 sp P00961 SYGB_ECOLI - GLYCYL- TRNA SYNTHETASE BETA CHAIN (GLYCINE-- TRNA LIGASE BETA CHAIN) (GLYRS)		UNCLASSIFIED	1003

4325	11359873 (18683, 18684)	Novel Protein sim. GBank gil586496 sp P38235 YBQ3_YEAST - HYPOTHETICAL 40.3 KD PROTEIN IN REG2- YRO2 INTERGENIC REGION	UNCLASSIFIED	1006
4326	78792061 (5865, 5866)	Novel Protein sim. GBank gil586504 sp P38241 YBR5_YEAST - HYPOTHETICAL 40.9 KD PROTEIN IN ORC2- TIP1 INTERGENIC REGION	UNCLASSIFIED	1009
4327	80248150 (16183, 16184)	Novel Protein sim. GBank gil586517 sp P38250 YBT6_YEAST - HYPOTHETICAL 105.9 KD PROTEIN IN AAC3- RFC5 INTERGENIC REGION	UNCLASSIFIED	1003, 1006, 1009, 1031, 1034, 1039
4328	79439310 (10891, 10892)	Novel Protein sim. GBank gil586528 sp P38261 YBV2_YEAST - HYPOTHETICAL 85.5 KD PROTEIN IN VPS15- YMC2 INTERGENIC REGION	UNCLASSIFIED	1034
4329	18598518 (11171, 11172)	Novel Protein sim. GBank gil586330 sp P38263 YBV5_YEAST - HYPOTHETICAL 41.2 KD PROTEIN IN YMC2- CMD1 INTERGENIC REGION	UNCLASSIFIED	1023
4330	28782605 (4771, 4772)	Novel Protein sim. GBank gil586533 sp P38266 YBV8_YEAST - HYPOTHETICAL 92.8 KD PROTEIN IN YMC2- CMD1 INTERGENIC REGION	UNCLASSIFIED	1026
4331	19887696 (14247, 14248)	Novel Protein sim. GBank gil586870 sp P37540 HOLB_BACSU - DNA POLYMERASE III, DELTA' SUBUNIT	UNCLASSIFIED	1034
4332	79205017 (2773, 2774)	Novel Protein sim. GBank gil586876 sp P37546 YABE_BACSU - HYPOTHETICAL 47.7 KD PROTEIN IN METS- KSGA INTERGENIC REGION	UNCLASSIFIED	1054
4333	27981381 (3129, 3130)	Novel Protein sim. GBank gil586877 sp P37547 YABF_BACSU - HYPOTHETICAL 20.7 KD PROTEIN IN METS- KSGA INTERGENIC REGION	UNCLASSIFIED	1006

4334	80062555 (19417, 19418)	Novel Protein sim. GBank gij625182 (L39015) - mitochondrial glutamyl-tRNA synthetase [Saccharomyces cerevisiae]	UNCLASSIFIED	1010
4335	39723336 (13767, 13768)	Novel Protein sim. GBank gij625184 (L38957) - mitochondrial isoleucyl-tRNA synthetase [Saccharomyces cerevisiae]	UNCLASSIFIED	1050
4336	33183575 (5793, 5794)	Novel Protein sim. GBank gij626375 [pir]S48472 - probable membrane protein YIL100c-a - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1026
4337	27982609 (14557, 14558)	Novel Protein sim. GBank gij626441 [pir]S48569 - hypothetical protein YLR219w - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1034
4338	39402485 (5407, 5408)	Novel Protein sim. GBank gij626642 [pir]S46723 - arginine-tRNA ligase (EC 6.1.1.19), mitochondrial - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1004, 1006, 1016, 1022, 1024
4339	79858563 (14529, 14530)	Novel Protein sim. GBank gij628110 [pir]S32975 - hypothetical protein - human herpesvirus 4	UNCLASSIFIED	1023
4340	39564742 (7519, 7520)	Novel Protein sim. GBank gij628710 [pir]S41739 - hypothetical protein - Escherichia coli	UNCLASSIFIED	1004
4341	10218925 (7227, 7228)	Novel Protein sim. GBank gij630472 [pir]A54138 - acidic repetitive protein arp1 - Tetrahymena thermophila (SGC5)	UNCLASSIFIED	1039
4342	94675524 (2759, 2760)	Novel Protein sim. GBank gij66457 [pir]XYP57A - site-specific DNA-methyltransferase (adenine-specific) (EC 2.1.1.72) Paer71 - Pseudomonas aeruginosa plasmid pMG7	UNCLASSIFIED	1022
4343	38922016 (1179, 1180)	Novel Protein sim. GBank gij683778 [emb]CAA88374] - (Z48483) unknown [Saccharomyces cerevisiae]	UNCLASSIFIED	1008
4344	78043821 (2275, 2276)	Novel Protein sim. GBank gij68563 [pir]YFBSB - phenylalanine-tRNA ligase (EC 6.1.1.20) beta chain - Bacillus subtilis	UNCLASSIFIED	1054

4345	19872489 (17983, 17984)	Novel Protein sim. GBank gi 68563 pir YFBSB - phenylalanine-tRNA ligase (EC 6.1.1.20) beta chain - <i>Bacillus subtilis</i>	UNCLASSIFIED	1034
4346	80423236 (18755, 18756)	Novel Protein sim. GBank gi 688011 bbs 155930 - (S73498) AgX-1 antigen [human, infertile patient, testis, Peptide, 505 aa] [Homo sapiens]	UNCLASSIFIED	1008, 1023, 1024, 1025, 1039, 1044
4347	29243304 (1507, 1508)	Novel Protein sim. GBank gi 699144 (U15180) - DNA-3-methyladenine glycosidase I [Mycobacterium leprae]	UNCLASSIFIED	1026
4348	47661876 (18273, 18274)	Novel Protein sim. GBank gi 699161 (U15181) - hypothetical protein [Mycobacterium leprae]	UNCLASSIFIED	1029
4349	78475888 (7823, 7824)	Novel Protein sim. GBank gi 727399 gb AAB65881 - (U22837) HmsH [Yersinia pestis]	UNCLASSIFIED	1003
4350	30407690 (11585, 11586)	Novel Protein sim. GBank gi 728659 emb CAA885271 - (Z48613) unknown [Saccharomyces cerevisiae]	UNCLASSIFIED	1008
4351	78674094 (3323, 3324)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII	UNCLASSIFIED	1026
4352	86671150 (4579, 4580)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII	UNCLASSIFIED	1007, 1019
4353	87128324 (5383, 5384)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII	UNCLASSIFIED	1025, 1026
4354	17958326 (7329, 7330)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII	UNCLASSIFIED	1016
4355	16375835 (7945, 7946)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII	UNCLASSIFIED	1054
4356	91231298 (8513, 8514)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII	UNCLASSIFIED	1010

4357	86668127 (9723, 9724)	Novel Protein sim. GBank gii728831 sp P39188 ALU1_HUMAN - III ALU SUBFAMILY J WARNING ENTRY III		UNCLASSIFIED	1008, 1029
4358	49320730 (11981, 11982)	Novel Protein sim. GBank gii728831 sp P39188 ALU1_HUMAN - III ALU SUBFAMILY J WARNING ENTRY III		UNCLASSIFIED	1040
4359	91226056 (12073, 12074)	Novel Protein sim. GBank gii728831 sp P39188 ALU1_HUMAN - III ALU SUBFAMILY J WARNING ENTRY III		UNCLASSIFIED	1010
4360	10141581 (12539, 12540)	Novel Protein sim. GBank gii728831 sp P39188 ALU1_HUMAN - III ALU SUBFAMILY J WARNING ENTRY III		UNCLASSIFIED	1025
4361	54531534 (12605, 12606)	Novel Protein sim. GBank gii728831 sp P39188 ALU1_HUMAN - III ALU SUBFAMILY J WARNING ENTRY III		UNCLASSIFIED	1041
4362	78486472 (13833, 13834)	Novel Protein sim. GBank gii728831 sp P39188 ALU1_HUMAN - III ALU SUBFAMILY J WARNING ENTRY III		UNCLASSIFIED	1026
4363	78890237 (15625, 15626)	Novel Protein sim. GBank gii728831 sp P39188 ALU1_HUMAN - III ALU SUBFAMILY J WARNING ENTRY III		UNCLASSIFIED	1024
4364	37016371 (16081, 16082)	Novel Protein sim. GBank gii728831 sp P39188 ALU1_HUMAN - III ALU SUBFAMILY J WARNING ENTRY III		UNCLASSIFIED	1025
4365	79775055 (18705, 18706)	Novel Protein sim. GBank gii728831 sp P39188 ALU1_HUMAN - III ALU SUBFAMILY J WARNING ENTRY III		UNCLASSIFIED	1003, 1023, 1044
4366	13520123 (20591, 20592)	Novel Protein sim. GBank gii728831 sp P39188 ALU1_HUMAN - III ALU SUBFAMILY J WARNING ENTRY III		UNCLASSIFIED	1024
4367	90935104 (20959, 20960)	Novel Protein sim. GBank gii728831 sp P39188 ALU1_HUMAN - III ALU SUBFAMILY J WARNING ENTRY III		UNCLASSIFIED	1020
4368	54536980 (21533, 21534)	Novel Protein sim. GBank gii728831 sp P39188 ALU1_HUMAN - III ALU SUBFAMILY J WARNING ENTRY III		UNCLASSIFIED	1041

4369	66525975 (22005, 22006)	Novel Protein sim. GBank gil728831 splP39189 ALU1_HUMAN - III ALU SUBFAMILY J WARNING ENTRY III		UNCLASSIFIED	1022, 1038, 1054
4370	10128936 (6717, 6718)	Novel Protein sim. GBank gil728832 splP39189 ALU2_HUMAN - III ALU SUBFAMILY SB WARNING ENTRY III		UNCLASSIFIED	1025
4371	78675523 (16479, 16480)	Novel Protein sim. GBank gil728832 splP39189 ALU2_HUMAN - III ALU SUBFAMILY SB WARNING ENTRY III		UNCLASSIFIED	1026
4372	77918603 (20741, 20742)	Novel Protein sim. GBank gil728832 splP39189 ALU2_HUMAN - III ALU SUBFAMILY SB WARNING ENTRY III		UNCLASSIFIED	1019, 1036
4373	79844234 (7229, 7230)	Novel Protein sim. GBank gil728835 splP39192 ALU5_HUMAN - III ALU SUBFAMILY SC WARNING ENTRY III		UNCLASSIFIED	1044
4374	71329591 (13295, 13296)	Novel Protein sim. GBank gil728836 splP39193 ALU6_HUMAN - III ALU SUBFAMILY SP WARNING ENTRY III		UNCLASSIFIED	1026, 1050
4375	78282764 (8865, 8866)	Novel Protein sim. GBank gil728837 splP39194 ALU7_HUMAN - III ALU SUBFAMILY SQ WARNING ENTRY III		UNCLASSIFIED	1029
4376	46691574 (17919, 17920)	Novel Protein sim. GBank gil728837 splP39194 ALU7_HUMAN - III ALU SUBFAMILY SQ WARNING ENTRY III		UNCLASSIFIED	1055
4377	18403567 (20451, 20452)	Novel Protein sim. GBank gil728837 splP39194 ALU7_HUMAN - III ALU SUBFAMILY SQ WARNING ENTRY III		UNCLASSIFIED	1004
4378	27369084 (21417, 21418)	Novel Protein sim. GBank gil728837 splP39194 ALU7_HUMAN - III ALU SUBFAMILY SQ WARNING ENTRY III		UNCLASSIFIED	1026
4379	79558315 (4777, 4778)	Novel Protein sim. GBank gil728838 splP39195 ALU8_HUMAN - III ALU SUBFAMILY SX WARNING ENTRY III		UNCLASSIFIED	1023

4380	95199241 (16767, 16768)	Novel Protein sim. GBank gij728850 sp P08640 AMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4- ALPHA-D-GLUCAN GLUCOHYDROLASE)		UNCLASSIFIED	1027, 1029
4381	78776077 (16277, 16278)	Novel Protein sim. GBank gij728868 sp P40603 APG_BRANA - ANTER- SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)		UNCLASSIFIED	1009, 1017
4382	78908326 (18211, 18212)	Novel Protein sim. GBank gij728868 sp P40603 APG_BRANA - ANTER- SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)		UNCLASSIFIED	1044
4383	82062189 (6407, 6408)	Novel Protein sim. GBank gij729352 sp P32354 DN43_YEAST - DNA43 PROTEIN		UNCLASSIFIED	1003, 1004, 1006, 1010, 1012, 1016, 1022, 1023, 1024, 1029, 1034, 1038
4384	80464569 (381, 382)	Novel Protein sim. GBank gij729534 sp P21373 UTR1_YEAST - UTR1 PROTEIN (UNKNOWN TRANSCRIPT 1 PROTEIN)		UNCLASSIFIED	1008, 1010, 1012, 1017, 1022, 1023, 1030, 1034, 1038, 1039, 1044
4385	20702426 (22225, 22226)	Novel Protein sim. GBank gij729721 sp P07172 HIS8_YEAST - HISTIDINOL- PHOSPHATE AMINOTRANSFERASE (IMIDAZOLE ACETOL-PHOSPHATE TRANSAMINASE)		UNCLASSIFIED	1022
4386	20438387 (701, 702)	Novel Protein sim. GBank gij729747 sp P39662 HMPA_ALCEU - FLAVOHEMOPROTEIN (HAEMOGLOBIN-LIKE PROTEIN) (FLAVOHEMOGLOBIN)		UNCLASSIFIED	1010
4387	78747957 (4401, 4402)	Novel Protein sim. GBank gij730197 sp P40354 NTA1_YEAST - PROTEIN N- TERMINAL AMIDASE (NT-AMIDASE)		UNCLASSIFIED	1044

4388	38922472 (20645, 20646)	Novel Protein sim. GBank gi 730779 sp P38904 SP41_YEAST - SPP41 PROTEIN		UNCLASSIFIED	1008
4389	79853762 (15439, 15440)	Novel Protein sim. GBank gi 730887 sp P08956 T1R_ECOLI - TYPE I RESTRICTION ENZYME ECK1R PROTEIN		UNCLASSIFIED	1044
4390	71760881 (275, 276)	Novel Protein sim. GBank gi 730888 sp Q06666 T2_MOUSE - OCTAPEPTIDE-REPEAT PROTEIN T2		UNCLASSIFIED	1008
4391	78460840 (12843, 12844)	Novel Protein sim. GBank gi 730986 sp P41068 TRAP_ECOLI - TRAP PROTEIN		UNCLASSIFIED	1044
4392	27974366 (16869, 16870)	Novel Protein sim. GBank gi 731010 sp Q00188 TRL4_ECOLI - TRAL PROTEIN		UNCLASSIFIED	1022
4393	71844493 (9191, 9192)	Novel Protein sim. GBank gi 731303 sp P27637 YA14_YEAST - HYPOTHETICAL 78.3 KD PROTEIN IN SEN34- ADE1 INTERGENIC REGION		UNCLASSIFIED	1022
4394	29242614 (20073, 20074)	Novel Protein sim. GBank gi 731367 sp P38962 YD66_YEAST - HYPOTHETICAL 23.1 KD PROTEIN IN STN1- AFR1 INTERGENIC REGION		UNCLASSIFIED	1017
4395	30263127 (6229, 6230)	Novel Protein sim. GBank gi 731404 sp P39996 YEB7_YEAST - HYPOTHETICAL 38.2 KD PROTEIN IN PMP2- VAC8 INTERGENIC REGION		UNCLASSIFIED	1008
4396	10166025 (11565, 11566)	Novel Protein sim. GBank gi 731434 sp P40008 YEJ4_YEAST - HYPOTHETICAL 25.1 KD PROTEIN IN PMI40- PAC2 INTERGENIC REGION		UNCLASSIFIED	1024
4397	79611412 (10225, 10226)	Novel Protein sim. GBank gi 731524 sp P40090 YEX7_YEAST - HYPOTHETICAL 72.1 KD PROTEIN IN FTR1- SPT15 INTERGENIC REGION		UNCLASSIFIED	1008

4398	30604031 (1381, 1382)	Novel Protein sim. GBank gi 731525 sp P40091 PEA2_YEAST - PEA2 PROTEIN (PPF2 PROTEIN)		UNCLASSIFIED	1022
4399	27926460 (20727, 20728)	Novel Protein sim. GBank gi 731530 sp P40095 YFY8_YEAST - HYPOTHETICAL 63.7 KD PROTEIN IN BEM2- NCB1 INTERGENIC REGION		UNCLASSIFIED	1022
4400	71845439 (4597, 4598)	Novel Protein sim. GBank gi 731580 sp P38894 FLO5_YEAST - FLOCCULATION PROTEIN FLO5 PRECURSOR (FLOCCULIN 5)		UNCLASSIFIED	1022
4401	29264714 (20439, 20440)	Novel Protein sim. GBank gi 731604 sp P38742 YHC3_YEAST - HYPOTHETICAL 130.0 KD PROTEIN IN SNF6- SPO11 INTERGENIC REGION		UNCLASSIFIED	1003, 1004, 1006, 1022, 1024, 1034
4402	82457087 (12377, 12378)	Novel Protein sim. GBank gi 731672 sp P38793 YHN0_YEAST - HYPOTHETICAL 56.5 KD PROTEIN IN DYS1- ERG7 INTERGENIC REGION		UNCLASSIFIED	1001, 1003, 1004, 1006, 1008, 1009, 1010, 1012, 1017, 1022, 1023, 1024, 1026, 1031, 1034, 1039, 1044, 1050
4403	11354327 (9927, 9928)	Novel Protein sim. GBank gi 731678 sp P38799 YHN8_YEAST - HYPOTHETICAL 63.3 KD PROTEIN IN NMD2- IRE1 INTERGENIC REGION		UNCLASSIFIED	1058
4404	80250819 (5231, 5232)	Novel Protein sim. GBank gi 731680 sp P38801 YHO1_YEAST - HYPOTHETICAL 21.0 KD PROTEIN IN IRE1- KSP1 INTERGENIC REGION		UNCLASSIFIED	1001, 1006, 1012, 1022, 1024, 1027, 1038, 1044
4405	56117620 (17131, 17132)	Novel Protein sim. GBank gi 731726 sp P32900 YHU9_YEAST - HYPOTHETICAL 81.8 KD PROTEIN IN MRPL6- SPO12 INTERGENIC REGION		UNCLASSIFIED	1008, 1030

4406	80430434 (4527, 4528)	Novel Protein sim. GBank gil731727 sp P38848 YHV0_YEAST - HYPOTHETICAL 66.1 KD PROTEIN IN MRPL6- SPO12 INTERGENIC REGION		UNCLASSIFIED	1001, 1003, 1004, 1006, 1008, 1009, 1010, 1016, 1022, 1024, 1025, 1031, 1034, 1038, 1039, 1040, 1054
4407	29684180 (14571, 14572)	Novel Protein sim. GBank gil731737 sp P38858 SOL3_YEAST - SOL3 PROTEIN		UNCLASSIFIED	1009
4408	34114340 (7241, 7242)	Novel Protein sim. GBank gil731739 sp P38860 YHW8_YEAST - HYPOTHETICAL 55.5 KD GTP-BINDING PROTEIN IN CDC23-DBP8 INTERGENIC REGION		UNCLASSIFIED	1000
4409	78729008 (17649, 17650)	Novel Protein sim. GBank gil731757 sp P38874 IKI1_YEAST - IKI1 PROTEIN		UNCLASSIFIED	1008
4410	57292758 (4403, 4404)	Novel Protein sim. GBank gil731758 sp P38875 YHY8_YEAST - HYPOTHETICAL 67.8 KD PROTEIN IN IKI1- ERG9 INTERGENIC REGION		UNCLASSIFIED	1001, 1009, 1022, 1024, 1026
4411	21418073 (17393, 17394)	Novel Protein sim. GBank gil731779 sp P40552 YIB1_YEAST - HYPOTHETICAL 26.3 KD PROTEIN IN PDR11- FAA3 INTERGENIC REGION		UNCLASSIFIED	1004
4412	20732337 (19551, 19552)	Novel Protein sim. GBank gil731805 sp P40528 SYG1_YEAST - SYG1 PROTEIN		UNCLASSIFIED	1010
4413	27849057 (16197, 16198)	Novel Protein sim. GBank gil731813 sp P40523 YIF5_YEAST - HYPOTHETICAL 70.7 KD PROTEIN IN SNP1- GPP1 INTERGENIC REGION		UNCLASSIFIED	1022, 1034

4414	17123843 (22029, 22030)	Novel Protein sim. GBank gil731813 splP40523 YIF5_YEAST - HYPOTHETICAL 70.7 KD PROTEIN IN SNP1- GPP1 INTERGENIC REGION		UNCLASSIFIED	1017
4415	78770255 (22693, 22694)	Novel Protein sim. GBank gil731815 splP40188 YIF7_YEAST - HYPOTHETICAL 19.2 KD PROTEIN IN SNP1- GPP1 INTERGENIC REGION		UNCLASSIFIED	1003, 1008, 1009, 1022
4416	95293324 (18567, 18568)	Novel Protein sim. GBank gil731821 splP40517 YIG3_YEAST - HYPOTHETICAL 36.1 KD PROTEIN IN RNR3- ARC15 INTERGENIC REGION		UNCLASSIFIED	1004, 1022, 1024
4417	71808933 (14585, 14586)	Novel Protein sim. GBank gil731842 splP40498 YJ1_YEAST - HYPOTHETICAL 84.0 KD PROTEIN IN SGA1- KTR7 INTERGENIC REGION		UNCLASSIFIED	1008, 1022
4418	78910859 (9217, 9218)	Novel Protein sim. GBank gil731850 splP40489 YIK1_YEAST - HYPOTHETICAL 72.7 KD PROTEIN IN MOB1- SGA1 INTERGENIC REGION		UNCLASSIFIED	1003
4419	78911074 (21719, 21720)	Novel Protein sim. GBank gil731853 splP40486 YIK4_YEAST - HYPOTHETICAL 59.2 KD PROTEIN IN MOB1- SGA1 INTERGENIC REGION		UNCLASSIFIED	1003, 1008
4420	25146202 (20849, 20850)	Novel Protein sim. GBank gil731862 splP40477 N159_YEAST - NUCLEOPORIN NUP159 (NUCLEAR PORE PROTEIN NUP159)		UNCLASSIFIED	1026
4421	80078065 (11065, 11066)	Novel Protein sim. GBank gil731864 splP40475 YIM0_YEAST - HYPOTHETICAL 61.8 KD PROTEIN IN KGD1- SIM1 INTERGENIC REGION		UNCLASSIFIED	1017, 1022, 1034
4422	79556341 (2895, 2896)	Novel Protein sim. GBank gil731871 splP40468 YIM9_YEAST - HYPOTHETICAL 269.9 KD PROTEIN IN FKH1- MET18 INTERGENIC REGION		UNCLASSIFIED	1025

4423	19883506 (14843, 14844)	Novel Protein sim. GBank gil731904 splP40561 YIS1_YEAST - HYPOTHETICAL 29.0 KD PROTEIN IN BET1- PAN1 INTERGENIC REGION		UNCLASSIFIED	1022
4424	80219116 (6983, 6984)	Novel Protein sim. GBank gil731935 splP40362 YJG9_YEAST - HYPOTHETICAL 66.4 KD PROTEIN IN SMC3- MRPL8 INTERGENIC REGION		UNCLASSIFIED	1006, 1009, 1010, 1022, 1024, 1034, 1039
4425	78675785 (4325, 4326)	Novel Protein sim. GBank gil731940 splP40367 YJG2_YEAST - HYPOTHETICAL 94.9 KD PROTEIN IN MRPL8- NUP82 INTERGENIC REGION		UNCLASSIFIED	1017
4426	79374109 (18553, 18554)	Novel Protein sim. GBank gil731940 splP40367 YJG2_YEAST - HYPOTHETICAL 94.9 KD PROTEIN IN MRPL8- NUP82 INTERGENIC REGION		UNCLASSIFIED	1003, 1022
4427	28806620 (719, 720)	Novel Protein sim. GBank gil731942 splP39526 YJU7_YEAST - HYPOTHETICAL 229.9 KD PROTEIN IN NUC1- NCE1 INTERGENIC REGION		UNCLASSIFIED	1004, 1022
4428	79588597 (22955, 22956)	Novel Protein sim. GBank gil731971 splP40856 S185_YEAST - SIT4- ASSOCIATING PROTEIN SAP185		UNCLASSIFIED	1022, 1024, 1026
4429	80059406 (7689, 7690)	Novel Protein sim. GBank gil732097 splP39389 YJIR_ECOLI - HYPOTHETICAL 53.0 KD PROTEIN IN IADA- MCRD INTERGENIC REGION (F470)		UNCLASSIFIED	1024, 1026
4430	79567067 (11507, 11508)	Novel Protein sim. GBank gil732104 splP39396 YJYI_ECOLI - HYPOTHETICAL 77.9 KD PROTEIN IN MRR- TSR INTERGENIC REGION (F721)		UNCLASSIFIED	1044
4431	80249658 (10519, 10520)	Novel Protein sim. GBank gil732167 splP40219 YM25_YEAST - HYPOTHETICAL 16.4 KD PROTEIN IN TIF34- SWP1 INTERGENIC REGION		UNCLASSIFIED	1003, 1022, 1024

4432	14995374 (14775, 14776)	Novel Protein sim. GBank gil732344 sp P39597 YVBN_BACSU - HYPOTHETICAL 45.7 KD PROTEIN IN EPR- GALK INTERGENIC REGION PRECURSOR		UNCLASSIFIED	1024
4433	24115247 (11387, 11388)	Novel Protein sim. GBank gil740613 prf 2005409A - rhodopsin [Alloteuthis subulita]		UNCLASSIFIED	1029
4434	80082341 (20837, 20838)	Novel Protein sim. GBank gil746474 (U23511) - weakly similar to dihydrokaempferol 4-reductase [Caenorhabditis elegans]		UNCLASSIFIED	1034
4435	20292082 (4133, 4134)	Novel Protein sim. GBank gil757830 emb CAA86044] - (Z37980) 2-oxo-hept- 3-ene-1,7-dioate hydratase [Escherichia coli]		UNCLASSIFIED	1024, 1034
4436	21425934 (7391, 7392)	Novel Protein sim. GBank gil758210 emb CAA55681] - (X79076) 2- halobenzoate 1,2-dioxygenase [Burkholderia cepacia]		UNCLASSIFIED	1022
4437	78766703 (13061, 13062)	Novel Protein sim. GBank gil76189 pir Q3ECBA - hypothetical 17K protein (bioA 3' region) - Escherichia coli		UNCLASSIFIED	1026
4438	79630475 (4837, 4838)	Novel Protein sim. GBank gil76204 pir Q4ECW7 - hypothetical protein 76 - Escherichia coli		UNCLASSIFIED	1039
4439	78769985 (22183, 22184)	Novel Protein sim. GBank gil763391 emb CAA52881] - (X74920) SNG1 [Saccharomyces cerevisiae]		UNCLASSIFIED	1026
4440	79250080 (9007, 9008)	Novel Protein sim. GBank gil773190 db BAA08787] - (D50083) BUL1 [Saccharomyces cerevisiae]		UNCLASSIFIED	1003, 1029
4441	25314591 (9347, 9348)	Novel Protein sim. GBank gil773190 db BAA08787] - (D50083) BUL1 [Saccharomyces cerevisiae]		UNCLASSIFIED	1009
4442	37030000 (3569, 3570)	Novel Protein sim. GBank gil790910 (L41861) - putative [Pseudomonas syringae]		UNCLASSIFIED	1038

4443	66177808 (4233, 4234)	Novel Protein sim. GBank gi 79557 pir S04678 - hypothetical protein 8 - Rhodopseudomonas blasticus (fragment)	UNCLASSIFIED	1022
4444	79618924 (10463, 10464)	Novel Protein sim. GBank gi 79973 pir S05542 - hypothetical protein, 54K - Enterococcus faecium	UNCLASSIFIED	1006
4445	16842116 (19533, 19534)	Novel Protein sim. GBank gi 807677 (M13101) - unknown protein [Rattus norvegicus]	UNCLASSIFIED	1008
4446	79253361 (22269, 22270)	Novel Protein sim. GBank gi 807677 (M13101) - unknown protein [Rattus norvegicus]	UNCLASSIFIED	1024
4447	78968384 (213, 214)	Novel Protein sim. GBank gi 81286 pir S22697 - extensin - Volvox carteri (fragment)	UNCLASSIFIED	1003
4448	28459036 (8915, 8916)	Novel Protein sim. GBank gi 81286 pir S22697 - extensin - Volvox carteri (fragment)	UNCLASSIFIED	1004, 1022, 1023, 1024, 1034
4449	78459239 (15465, 15466)	Novel Protein sim. GBank gi 81286 pir S22697 - extensin - Volvox carteri (fragment)	UNCLASSIFIED	1026
4450	79921163 (8027, 8028)	Novel Protein sim. GBank gi 825501 (L42348) - HOL1 [Saccharomyces cerevisiae]	UNCLASSIFIED	1008, 1023, 1039
4451	13502705 (1543, 1544)	Novel Protein sim. GBank gi 833812 (U21643) - high-affinity glutamine permease [Saccharomyces cerevisiae]	UNCLASSIFIED	1006
4452	81745594 (1969, 1970)	Novel Protein sim. GBank gi 840656 (L42524) - replication initiator and transcription repressor [Plasmodium falciparum]	UNCLASSIFIED	1054
4453	80026632 (9491, 9492)	Novel Protein sim. GBank gi 845686 (M32103) - ORF-27 [Staphylococcus aureus]	UNCLASSIFIED	1006, 1026, 1027, 1029, 1053
4454	65876460 (1123, 1124)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]	UNCLASSIFIED	1044
4455	79796417 (1189, 1190)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]	UNCLASSIFIED	1004, 1006, 1008, 1017, 1023, 1024, 1034, 1039, 1044, 1054
4456	37420757 (2709, 2710)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]	UNCLASSIFIED	1016

4457	20021358 (4955, 4956)	Novel Protein sim. GBank gii854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	1022
4458	28993067 (6277, 6278)	Novel Protein sim. GBank gii854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	1017
4459	10144718 (7217, 7218)	Novel Protein sim. GBank gii854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	1034
4460	78798207 (7601, 7602)	Novel Protein sim. GBank gii854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	1026
4461	65890895 (7633, 7634)	Novel Protein sim. GBank gii854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	1038
4462	79864042 (7831, 7832)	Novel Protein sim. GBank gii854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	1017
4463	80085583 (11203, 11204)	Novel Protein sim. GBank gii854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	1001
4464	55307020 (11849, 11850)	Novel Protein sim. GBank gii854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	1019
4465	10119836 (11897, 11898)	Novel Protein sim. GBank gii854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	1044
4466	32119969 (12717, 12718)	Novel Protein sim. GBank gii854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	1044
4467	19521359 (13535, 13536)	Novel Protein sim. GBank gii854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	1034
4468	80047867 (16109, 16110)	Novel Protein sim. GBank gii854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	1023, 1024

4469	78495393 (20715, 20716)	Novel Protein sim. GBank gil854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	1038
4470	79586116 (21721, 21722)	Novel Protein sim. GBank gil854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	1054
4471	65479236 (22503, 22504)	Novel Protein sim. GBank gil854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	1054
4472	80257959 (22603, 22604)	Novel Protein sim. GBank gil854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	1006
4473	81572628 (4435, 4436)	Novel Protein sim. GBank gil85719 pir A40333 - collagen alpha 1(II) chain precursor - African clawed frog		UNCLASSIFIED	1001, 1003, 1008, 1016, 1023, 1024, 1029, 1044, 1054
4474	46872841 (5797, 5798)	Novel Protein sim. GBank gil861277 (U28739) - C17G10.1 [Caenorhabditis elegans]		UNCLASSIFIED	1029
4475	80027717 (2523, 2524)	Novel Protein sim. GBank gil87765 pir JU0033 - hypothetical L1 protein (third intron of gene TS) - human		UNCLASSIFIED	1004
4476	87452835 (5429, 5430)	Novel Protein sim. GBank gil87765 pir JU0033 - hypothetical L1 protein (third intron of gene TS) - human		UNCLASSIFIED	1018
4477	78470339 (22567, 22568)	Novel Protein sim. GBank gil882509 (U28377) - ORF_3274 [Escherichia coli]		UNCLASSIFIED	1026
4478	80250942 (1139, 1140)	Novel Protein sim. GBank gil882649 (U29579) - ORF_199 [Escherichia coli]		UNCLASSIFIED	1022, 1024
4479	79801250 (9887, 9888)	Novel Protein sim. GBank gil886038 (U24659) - JadR1 [Streptomyces venezuelae]		UNCLASSIFIED	1017
4480	80481695 (18875, 18876)	Novel Protein sim. GBank gil886319 (L39923) - ORF278; hypothetical 30.3 Kd protein; similar to hypothetical protein 27.5 kd in SPO0J-GIDB intergenic region of B. subtilis and to 27.5 kd protein in GIDB-UNCI intergenic region of P. putida; putative [Mycobacterium leprae]		UNCLASSIFIED	1012

4481	8373624 (16975, 16976)	Novel Protein sim. GBank gi887833 (U28375) - ORF_0439 [Escherichia coli]	UNCLASSIFIED	1010
4482	78834904 (6181, 6182)	Novel Protein sim. GBank gi90157 pir A25345 - troponin T, cardiac muscle, major isoform - rabbit	UNCLASSIFIED	1003, 1026
4483	80402736 (13531, 13532)	Novel Protein sim. GBank gi91210 pir B24264 - proline-rich protein MP3 - mouse (fragment)	UNCLASSIFIED	1019, 1021, 1029
4484	27977012 (22485, 22486)	Novel Protein sim. GBank gi950682 (L38824) - putative [Plasmid R478]	UNCLASSIFIED	1022
4485	20466532 (10357, 10358)	Novel Protein sim. GBank gi95469 pir C33830 - cation efflux system membrane protein czcC - <i>Alcaligenes eutrophus</i>	UNCLASSIFIED	1010
4486	85805102 (18595, 18596)	Novel Protein sim. GBank gi95690 pir S14411 - carbon starvation protein - <i>Escherichia coli</i>	UNCLASSIFIED	1008, 1054
4487	18589572 (11211, 11212)	Novel Protein sim. GBank gi96522 pir A36129 - trigger factor - <i>Escherichia coli</i>	UNCLASSIFIED	1017
4488	11090399 (2769, 2770)	Novel Protein sim. GBank gi973332 (U30873) - OrfC [<i>Bacillus subtilis</i>]	UNCLASSIFIED	1006
4489	65680528 (17141, 17142)	Novel Protein sim. GBank gi97476 pir S19740 - hypothetical protein B - <i>Rhodobacter capsulatus</i>	UNCLASSIFIED	1010
4490	20438222 (5273, 5274)	Novel Protein sim. GBank gi97480 pir S19739 - integral membrane protein - <i>Rhodobacter capsulatus</i>	UNCLASSIFIED	1010
4491	78399485 (10821, 10822)	Novel Protein sim. GBank gi984814 (U27196) - zinc finger protein [Gallus gallus]	UNCLASSIFIED	1038
4492	20285233 (11621, 11622)	Novel Protein sim. GBank gi98773 pir S22630 - 19K antigen - <i>Mycobacterium intracellulare</i>	UNCLASSIFIED	1034
4493	80245788 (9659, 9660)	Novel Protein sim. GBank gi98810 pir S21833 - hypothetical protein - <i>Mycobacterium tuberculosis</i>	UNCLASSIFIED	1004, 1006, 1022, 1024, 1044, 1050
4494	79833913 (2961, 2962)	Novel Protein sim. GBank gi995573 (U03772) - putative transposase [Acinetobacter sp. ADP1]	UNCLASSIFIED	1008
4495	11269481 (9641, 9642)	Novel Protein sim. GBank gi995714 emb CAA62663 - (X91258) L3177 [<i>Saccharomyces cerevisiae</i>]	UNCLASSIFIED	1010
4496	9848880 (5, 6)		UNCLASSIFIED	1008

4497	65493874 (13, 14)			UNCLASSIFIED	1023
4498	29249693 (19, 20)			UNCLASSIFIED	1026
4499	35066762 (27, 28)			UNCLASSIFIED	1054
4500	20287804 (31, 32)			UNCLASSIFIED	1034
4501	86689310 (39, 40)			UNCLASSIFIED	1001, 1025
4502	78491874 (47, 48)			UNCLASSIFIED	1054
4503	25264471 (53, 54)			UNCLASSIFIED	1039
4504	79796056 (61, 62)			UNCLASSIFIED	1044
4505	79634543 (79, 80)			UNCLASSIFIED	1025
4506	20617182 (85, 86)			UNCLASSIFIED	1004
4507	79183388 (87, 88)			UNCLASSIFIED	1031
4508	70437139 (91, 92)			UNCLASSIFIED	1041
4509	38905642 (93, 94)			UNCLASSIFIED	1026
4510	80481704 (95, 96)			UNCLASSIFIED	1012
4511	94323105 (101, 102)			UNCLASSIFIED	1054
4512	94137362 (103, 104)			UNCLASSIFIED	1013, 1042, 1044
4513	17884908 (109, 110)			UNCLASSIFIED	1024
4514	38069116 (111, 112)			UNCLASSIFIED	1054

4515	65689631 (113, 114)			UNCLASSIFIED	1053
4516	79600369 (115, 116)			UNCLASSIFIED	1006
4517	76380394 (121, 122)			UNCLASSIFIED	1008, 1026, 1029
4518	29681396 (129, 130)			UNCLASSIFIED	1038
4519	27975422 (145, 146)			UNCLASSIFIED	1053
4520	20417383 (149, 150)			UNCLASSIFIED	1004
4521	49609065 (155, 156)			UNCLASSIFIED	1040
4522	30797666 (157, 158)			UNCLASSIFIED	1026
4523	39527189 (161, 162)			UNCLASSIFIED	1006
4524	11685039 (163, 164)			UNCLASSIFIED	1016
4525	79638103 (169, 170)			UNCLASSIFIED	1025, 1038
4526	85818238 (171, 172)			UNCLASSIFIED	1019
4527	65464571 (173, 174)			UNCLASSIFIED	1049
4528	25259756 (177, 178)			UNCLASSIFIED	1008
4529	36897891 (203, 204)			UNCLASSIFIED	1030
4530	66435382 (207, 208)			UNCLASSIFIED	1024
4531	35902288 (221, 222)			UNCLASSIFIED	1029
4532	79585126 (225, 226)			UNCLASSIFIED	1022

4533	11104197 (241, 242)			UNCLASSIFIED	1053
4534	17899010 (247, 248)			UNCLASSIFIED	1023
4535	27348004 (249, 250)			UNCLASSIFIED	1009
4536	79777084 (251, 252)			UNCLASSIFIED	1006, 1008
4537	30784847 (261, 262)			UNCLASSIFIED	1003
4538	94853854 (285, 286)			UNCLASSIFIED	1010, 1054
4539	10866996 (299, 300)			UNCLASSIFIED	1034
4540	27965979 (305, 306)			UNCLASSIFIED	1006
4541	17089664 (315, 316)			UNCLASSIFIED	1038
4542	70445891 (347, 348)			UNCLASSIFIED	1021, 1041
4543	66489680 (359, 360)			UNCLASSIFIED	1029
4544	79625154 (361, 362)			UNCLASSIFIED	1009, 1039
4545	87466598 (367, 368)			UNCLASSIFIED	1015
4546	20730941 (389, 390)			UNCLASSIFIED	1006
4547	78245845 (391, 392)			UNCLASSIFIED	1050
4548	43155273 (399, 400)			UNCLASSIFIED	1037
4549	77879730 (401, 402)			UNCLASSIFIED	1019
4550	65892848 (403, 404)			UNCLASSIFIED	1054

4551	16335049 (423, 424)			UNCLASSIFIED	1006
4552	77876576 (429, 430)			UNCLASSIFIED	1019
4553	55402072 (453, 454)			UNCLASSIFIED	1019
4554	78675447 (459, 460)			UNCLASSIFIED	1008
4555	57302106 (483, 484)			UNCLASSIFIED	1006, 1024
4556	20728641 (485, 486)			UNCLASSIFIED	1006
4557	78793908 (487, 488)			UNCLASSIFIED	1009
4558	65448002 (493, 494)			UNCLASSIFIED	1009
4559	78195745 (495, 496)			UNCLASSIFIED	1029
4560	79975683 (505, 506)			UNCLASSIFIED	1025
4561	11090550 (511, 512)			UNCLASSIFIED	1006
4562	32094039 (513, 514)			UNCLASSIFIED	1044
4563	79858796 (527, 528)			UNCLASSIFIED	1023
4564	78925935 (529, 530)			UNCLASSIFIED	1039
4565	32444528 (531, 532)			UNCLASSIFIED	1029
4566	27977688 (539, 540)			UNCLASSIFIED	1006
4567	80062542 (543, 544)			UNCLASSIFIED	1010
4568	66936028 (545, 546)			UNCLASSIFIED	1019, 1049

4569	8474093 (553, 554)			UNCLASSIFIED	1034
4570	29357849 (569, 570)			UNCLASSIFIED	1023
4571	20635625 (573, 574)			UNCLASSIFIED	1022
4572	11090554 (601, 602)			UNCLASSIFIED	1006
4573	38191553 (605, 606)			UNCLASSIFIED	1008
4574	13085136 (607, 608)			UNCLASSIFIED	1024
4575	79549190 (611, 612)			UNCLASSIFIED	1038
4576	20433843 (641, 642)			UNCLASSIFIED	1024
4577	19431094 (649, 650)			UNCLASSIFIED	1003
4578	32601107 (651, 652)			UNCLASSIFIED	1034
4579	79561278 (693, 694)			UNCLASSIFIED	1038
4580	20462931 (713, 714)			UNCLASSIFIED	1001, 1034
4581	80093083 (715, 716)			UNCLASSIFIED	1054
4582	80034797 (723, 724)			UNCLASSIFIED	1053
4583	55308623 (729, 730)			UNCLASSIFIED	1012, 1042
4584	71088722 (731, 732)			UNCLASSIFIED	1053
4585	35101923 (745, 746)			UNCLASSIFIED	1024
4586	10252060 (759, 760)			UNCLASSIFIED	1038

4587	8517446 (765, 766)			UNCLASSIFIED	1022
4588	94315340 (767, 768)			UNCLASSIFIED	1003
4589	79592603 (769, 770)			UNCLASSIFIED	1010
4590	78299571 (775, 776)			UNCLASSIFIED	1026
4591	19887951 (787, 788)			UNCLASSIFIED	1001
4592	79954360 (793, 794)			UNCLASSIFIED	1025
4593	17302392 (795, 796)			UNCLASSIFIED	1008
4594	77654893 (805, 806)			UNCLASSIFIED	1024
4595	79624224 (813, 814)			UNCLASSIFIED	1023
4596	46806799 (817, 818)			UNCLASSIFIED	1041
4597	80066630 (829, 830)			UNCLASSIFIED	1024, 1054
4598	57666192 (831, 832)			UNCLASSIFIED	1051
4599	65896665 (835, 836)			UNCLASSIFIED	1054
4600	29213531 (849, 850)			UNCLASSIFIED	1044
4601	8487746 (877, 878)			UNCLASSIFIED	1022
4602	17690652 (879, 880)			UNCLASSIFIED	1039
4603	16841330 (885, 886)			UNCLASSIFIED	1044
4604	30258305 (911, 912)			UNCLASSIFIED	1008

4605	30243801 (927, 928)			UNCLASSIFIED	1026
4606	80188879 (937, 938)			UNCLASSIFIED	1022, 1058
4607	81777196 (961, 962)			UNCLASSIFIED	1003, 1010, 1024
4608	20610456 (981, 982)			UNCLASSIFIED	1004
4609	79578027 (985, 986)			UNCLASSIFIED	1006
4610	35606134 (997, 998)			UNCLASSIFIED	1053
4611	33711024 (1001, 1002)			UNCLASSIFIED	1034
4612	90937181 (1009, 1010)			UNCLASSIFIED	1008, 1017, 1020, 1054
4613	29444464 (1013, 1014)			UNCLASSIFIED	1026
4614	80216194 (1029, 1030)			UNCLASSIFIED	1010, 1017, 1023, 1034, 1039
4615	21417118 (1037, 1038)			UNCLASSIFIED	1034
4616	20293187 (1041, 1042)			UNCLASSIFIED	1034
4617	11689569 (1067, 1068)			UNCLASSIFIED	1034
4618	11594236 (1077, 1078)			UNCLASSIFIED	1034
4619	66396127 (1087, 1088)			UNCLASSIFIED	1008, 1050
4620	20294715 (1091, 1092)			UNCLASSIFIED	1034
4621	27826749 (1097, 1098)			UNCLASSIFIED	1004
4622	11311200 (1101, 1102)			UNCLASSIFIED	1004

4623	66432596 (1129, 1130)			UNCLASSIFIED	1003, 1024
4624	33188191 (1131, 1132)			UNCLASSIFIED	1026
4625	19515516 (1147, 1148)			UNCLASSIFIED	1010
4626	95287728 (1153, 1154)			UNCLASSIFIED	1012
4627	65687079 (1155, 1156)			UNCLASSIFIED	1049
4628	10318131 (1159, 1160)			UNCLASSIFIED	1025
4629	65507263 (1163, 1164)			UNCLASSIFIED	1016
4630	11090012 (1169, 1170)			UNCLASSIFIED	1004
4631	79207956 (1187, 1188)			UNCLASSIFIED	1054
4632	10167111 (1203, 1204)			UNCLASSIFIED	1001
4633	79111413 (1227, 1228)			UNCLASSIFIED	1008, 1023, 1039
4634	30802163 (1235, 1236)			UNCLASSIFIED	1029
4635	10184774 (1251, 1252)			UNCLASSIFIED	1003
4636	78368100 (1261, 1262)			UNCLASSIFIED	1008
4637	57108817 (1285, 1286)			UNCLASSIFIED	1001
4638	11171532 (1287, 1288)			UNCLASSIFIED	1022
4639	20617923 (1307, 1308)			UNCLASSIFIED	1022
4640	42942388 (1315, 1316)			UNCLASSIFIED	1000

4641	24135956 (1327, 1328)			UNCLASSIFIED	1009
4642	25133369 (1329, 1330)			UNCLASSIFIED	1003
4643	37013769 (1331, 1332)			UNCLASSIFIED	1029
4644	25266291 (1337, 1338)			UNCLASSIFIED	1003
4645	20632797 (1339, 1340)			UNCLASSIFIED	1004
4646	65897765 (1345, 1346)			UNCLASSIFIED	1054
4647	78902794 (1351, 1352)			UNCLASSIFIED	1044
4648	42392967 (1353, 1354)			UNCLASSIFIED	1037
4649	8720829 (1357, 1358)			UNCLASSIFIED	1053
4650	37030710 (1371, 1372)			UNCLASSIFIED	1038
4651	20619152 (1385, 1386)			UNCLASSIFIED	1004
4652	29916453 (1389, 1390)			UNCLASSIFIED	1024
4653	29498389 (1393, 1394)			UNCLASSIFIED	1009
4654	78252926 (1397, 1398)			UNCLASSIFIED	1026
4655	77593493 (1405, 1406)			UNCLASSIFIED	1023
4656	80207649 (1407, 1408)			UNCLASSIFIED	1034
4657	80428752 (1409, 1410)			UNCLASSIFIED	1038, 1039
4658	25167576 (1447, 1448)			UNCLASSIFIED	1023

4659	27972165 (1451, 1452)			UNCLASSIFIED	1006
4660	56303804 (1473, 1474)			UNCLASSIFIED	1016
4661	78254851 (1475, 1476)			UNCLASSIFIED	1026
4662	77706453 (1481, 1482)			UNCLASSIFIED	1044
4663	15031765 (1483, 1484)			UNCLASSIFIED	1054
4664	11359941 (1501, 1502)			UNCLASSIFIED	1006
4665	79866321 (1503, 1504)			UNCLASSIFIED	1038
4666	39564900 (1519, 1520)			UNCLASSIFIED	1022, 1024
4667	18234054 (1541, 1542)			UNCLASSIFIED	1024
4668	51820195 (1545, 1546)			UNCLASSIFIED	1040
4669	28799635 (1547, 1548)			UNCLASSIFIED	1022
4670	80236214 (1549, 1550)			UNCLASSIFIED	1006
4671	78908513 (1553, 1554)			UNCLASSIFIED	1003, 1039
4672	17890206 (1557, 1558)			UNCLASSIFIED	1025
4673	47656276 (1565, 1566)			UNCLASSIFIED	1029
4674	33204747 (1573, 1574)			UNCLASSIFIED	1026
4675	78467565 (1575, 1576)			UNCLASSIFIED	1008
4676	79584957 (1577, 1578)			UNCLASSIFIED	1054

4677	29946342 (1587, 1588)			UNCLASSIFIED	1038
4678	37015719 (1601, 1602)			UNCLASSIFIED	1029
4679	85544086 (1613, 1614)			UNCLASSIFIED	1016, 1034, 1038, 1041
4680	55404303 (1615, 1616)			UNCLASSIFIED	1021
4681	55658487 (1617, 1618)			UNCLASSIFIED	1042
4682	46873136 (1627, 1628)			UNCLASSIFIED	1050
4683	65880999 (1629, 1630)			UNCLASSIFIED	1054
4684	17682849 (1635, 1636)			UNCLASSIFIED	1039
4685	36824627 (1659, 1660)			UNCLASSIFIED	1054
4686	17702485 (1669, 1670)			UNCLASSIFIED	1003
4687	78733265 (1673, 1674)			UNCLASSIFIED	1026, 1050
4688	66155223 (1677, 1678)			UNCLASSIFIED	1003
4689	16345558 (1685, 1686)			UNCLASSIFIED	1022
4690	79252662 (1687, 1688)			UNCLASSIFIED	1003, 1023
4691	80390078 (1691, 1692)			UNCLASSIFIED	1001, 1017, 1024, 1029
4692	32573701 (1709, 1710)			UNCLASSIFIED	1034
4693	54700090 (1715, 1716)			UNCLASSIFIED	1019
4694	10067522 (1727, 1728)			UNCLASSIFIED	1012

4695	79640542 (1731, 1732)			UNCLASSIFIED	1025
4696	35062253 (1733, 1734)			UNCLASSIFIED	1024
4697	13519751 (1743, 1744)			UNCLASSIFIED	1024
4698	80236216 (1745, 1746)			UNCLASSIFIED	1006, 1017
4699	94328999 (1759, 1760)			UNCLASSIFIED	1010
4700	78928034 (1767, 1768)			UNCLASSIFIED	1008, 1050
4701	85519710 (1773, 1774)			UNCLASSIFIED	1003, 1023, 1049, 1058
4702	78360920 (1785, 1786)			UNCLASSIFIED	1008, 1026
4703	78823898 (1789, 1790)			UNCLASSIFIED	1016, 1054
4704	54537001 (1797, 1798)			UNCLASSIFIED	1041
4705	94239569 (1799, 1800)			UNCLASSIFIED	1039
4706	35106845 (1809, 1810)			UNCLASSIFIED	1026
4707	20451074 (1817, 1818)			UNCLASSIFIED	1024
4708	36827848 (1819, 1820)			UNCLASSIFIED	1054
4709	79642387 (1827, 1828)			UNCLASSIFIED	1022, 1038
4710	19456885 (1833, 1834)			UNCLASSIFIED	1038
4711	10365133 (1843, 1844)			UNCLASSIFIED	1001
4712	70760933 (1847, 1848)			UNCLASSIFIED	1034

4713	80025927 (1855, 1856)			UNCLASSIFIED	1004, 1006, 1024, 1034
4714	79115173 (1871, 1872)			UNCLASSIFIED	1003
4715	36921063 (1875, 1876)			UNCLASSIFIED	1026
4716	23291629 (1887, 1888)			UNCLASSIFIED	1003
4717	38879543 (1899, 1900)			UNCLASSIFIED	1019
4718	65890856 (1903, 1904)			UNCLASSIFIED	1038
4719	35062838 (1909, 1910)			UNCLASSIFIED	1024
4720	38909591 (1937, 1938)			UNCLASSIFIED	1024
4721	65488001 (1943, 1944)			UNCLASSIFIED	1023
4722	29207312 (1947, 1948)			UNCLASSIFIED	1030
4723	80407444 (1965, 1966)			UNCLASSIFIED	1003, 1008, 1023, 1026, 1029, 1044, 1053
4724	21662567 (1999, 2000)			UNCLASSIFIED	1024, 1038, 1054
4725	29228558 (2021, 2022)			UNCLASSIFIED	1030
4726	79959396 (2023, 2024)			UNCLASSIFIED	1016
4727	79201769 (2029, 2030)			UNCLASSIFIED	1001, 1025, 1044, 1054
4728	20417013 (2057, 2058)			UNCLASSIFIED	1004
4729	20752080 (2067, 2068)			UNCLASSIFIED	1022
4730	79480166 (2069, 2070)			UNCLASSIFIED	1025

4731	20750859 (2071, 2072)			UNCLASSIFIED	1022
4732	16841981 (2083, 2084)			UNCLASSIFIED	1039
4733	78375158 (2085, 2086)			UNCLASSIFIED	1003
4734	80076596 (2095, 2096)			UNCLASSIFIED	1022
4735	80025928 (2099, 2100)			UNCLASSIFIED	1006, 1010, 1034
4736	29017297 (2103, 2104)			UNCLASSIFIED	1044
4737	30800379 (2109, 2110)			UNCLASSIFIED	1006
4738	78890648 (2123, 2124)			UNCLASSIFIED	1044
4739	78460233 (2125, 2126)			UNCLASSIFIED	1026
4740	66148000 (2151, 2152)			UNCLASSIFIED	1038
4741	91230908 (2159, 2160)			UNCLASSIFIED	1003
4742	46850003 (2161, 2162)			UNCLASSIFIED	1029
4743	71466607 (2167, 2168)			UNCLASSIFIED	1026
4744	16423261 (2177, 2178)			UNCLASSIFIED	1016
4745	39565694 (2181, 2182)			UNCLASSIFIED	1010
4746	10872205 (2189, 2190)			UNCLASSIFIED	1004
4747	79201928 (2199, 2200)			UNCLASSIFIED	1024
4748	78399033 (2201, 2202)			UNCLASSIFIED	1038

4749	36921068 (2205, 2206)			UNCLASSIFIED	1026
4750	78677359 (2215, 2216)			UNCLASSIFIED	1026
4751	71761302 (2221, 2222)			UNCLASSIFIED	1026
4752	17277231 (2223, 2224)			UNCLASSIFIED	1008
4753	78167568 (2225, 2226)			UNCLASSIFIED	1000
4754	78191615 (2227, 2228)			UNCLASSIFIED	1024
4755	20437153 (2231, 2232)			UNCLASSIFIED	1010
4756	17668990 (2241, 2242)			UNCLASSIFIED	1008
4757	29916352 (2251, 2252)			UNCLASSIFIED	1030
4758	78068607 (2261, 2262)			UNCLASSIFIED	1001
4759	29457545 (2271, 2272)			UNCLASSIFIED	1022
4760	54697548 (2273, 2274)			UNCLASSIFIED	1022
4761	34669099 (2279, 2280)			UNCLASSIFIED	1024
4762	25256289 (2283, 2284)			UNCLASSIFIED	1008
4763	79629028 (2291, 2292)			UNCLASSIFIED	1039
4764	41083545 (2295, 2296)			UNCLASSIFIED	1037
4765	19512872 (2297, 2298)			UNCLASSIFIED	1010
4766	94680343 (2307, 2308)			UNCLASSIFIED	1009, 1024, 1031

4767	8485740 (2309, 2310)			UNCLASSIFIED	1024
4768	77891859 (2313, 2314)			UNCLASSIFIED	1036
4769	65848664 (2315, 2316)			UNCLASSIFIED	1038
4770	65861051 (2331, 2332)			UNCLASSIFIED	1044
4771	11695127 (2339, 2340)			UNCLASSIFIED	1006
4772	86695575 (2349, 2350)			UNCLASSIFIED	1022, 1034, 1038
4773	91213648 (2367, 2368)			UNCLASSIFIED	1024
4774	80243819 (2385, 2386)			UNCLASSIFIED	1022, 1044
4775	27844078 (2387, 2388)			UNCLASSIFIED	1024, 1034
4776	20296623 (2391, 2392)			UNCLASSIFIED	1034
4777	79245600 (2409, 2410)			UNCLASSIFIED	1024, 1039
4778	78914507 (2411, 2412)			UNCLASSIFIED	1039
4779	12999306 (2415, 2416)			UNCLASSIFIED	1024
4780	38348356 (2425, 2426)			UNCLASSIFIED	1008
4781	11670394 (2431, 2432)			UNCLASSIFIED	1016, 1022
4782	80063162 (2449, 2450)			UNCLASSIFIED	1010, 1022, 1024, 1026, 1038
4783	79258057 (2477, 2478)			UNCLASSIFIED	1003
4784	11092879 (2479, 2480)			UNCLASSIFIED	1022

4785	11776390 (2483, 2484)			UNCLASSIFIED	1006
4786	65882019 (2491, 2492)			UNCLASSIFIED	1054
4787	51782563 (2499, 2500)			UNCLASSIFIED	1038, 1042
4788	78473417 (2515, 2516)			UNCLASSIFIED	1026
4789	87898974 (2537, 2538)			UNCLASSIFIED	1015, 1022, 1025
4790	9398491 (2539, 2540)			UNCLASSIFIED	1017
4791	28382878 (2541, 2542)			UNCLASSIFIED	1017
4792	20284772 (2545, 2546)			UNCLASSIFIED	1022
4793	11290122 (2557, 2558)			UNCLASSIFIED	1034
4794	25310199 (2567, 2568)			UNCLASSIFIED	1003
4795	86667225 (2571, 2572)			UNCLASSIFIED	1029
4796	20285338 (2579, 2580)			UNCLASSIFIED	1022
4797	79830272 (2581, 2582)			UNCLASSIFIED	1039
4798	11122661 (2587, 2588)			UNCLASSIFIED	1053
4799	78918477 (2597, 2598)			UNCLASSIFIED	1039
4800	20287821 (2599, 2600)			UNCLASSIFIED	1034
4801	23294346 (2601, 2602)			UNCLASSIFIED	1044
4802	95010589 (2605, 2606)			UNCLASSIFIED	1024, 1034, 1039

4803	65859051 (2607, 2608)			UNCLASSIFIED	1038
4804	34755701 (2609, 2610)			UNCLASSIFIED	1030
4805	42563732 (2611, 2612)			UNCLASSIFIED	1000, 1034
4806	65891738 (2613, 2614)			UNCLASSIFIED	1054
4807	11707335 (2619, 2620)			UNCLASSIFIED	1038
4808	86723575 (2625, 2626)			UNCLASSIFIED	1001, 1018
4809	47657344 (2641, 2642)			UNCLASSIFIED	1029
4810	87125822 (2659, 2660)			UNCLASSIFIED	1048
4811	21660817 (2661, 2662)			UNCLASSIFIED	1024
4812	30370208 (2673, 2674)			UNCLASSIFIED	1054
4813	12925917 (2689, 2690)			UNCLASSIFIED	1024
4814	78464624 (2715, 2716)			UNCLASSIFIED	1039
4815	78674394 (2739, 2740)			UNCLASSIFIED	1009
4816	79855987 (2741, 2742)			UNCLASSIFIED	1017, 1044
4817	65683598 (2743, 2744)			UNCLASSIFIED	1046
4818	79910981 (2745, 2746)			UNCLASSIFIED	1001, 1010, 1038
4819	65888420 (2747, 2748)			UNCLASSIFIED	1054
4820	65893010 (2765, 2766)			UNCLASSIFIED	1054

4821	78793103 (2805, 2806)			UNCLASSIFIED	1044
4822	79480342 (2807, 2808)			UNCLASSIFIED	1022
4823	86380873 (2813, 2814)			UNCLASSIFIED	1053
4824	87890180 (2815, 2816)			UNCLASSIFIED	1015
4825	29361964 (2823, 2824)			UNCLASSIFIED	1023
4826	79625167 (2847, 2848)			UNCLASSIFIED	1023
4827	80200419 (2861, 2862)			UNCLASSIFIED	1034
4828	51728608 (2873, 2874)			UNCLASSIFIED	1040
4829	65655505 (2889, 2890)			UNCLASSIFIED	1054
4830	10015425 (2909, 2910)			UNCLASSIFIED	1023
4831	24115887 (2911, 2912)			UNCLASSIFIED	1044
4832	11816407 (2915, 2916)			UNCLASSIFIED	1004
4833	78962233 (2919, 2920)			UNCLASSIFIED	1038
4834	80020135 (2921, 2922)			UNCLASSIFIED	1053
4835	37443826 (2927, 2928)			UNCLASSIFIED	1034
4836	30378685 (2943, 2944)			UNCLASSIFIED	1050
4837	30394718 (2945, 2946)			UNCLASSIFIED	1038
4838	27967298 (2951, 2952)			UNCLASSIFIED	1006

4839	79450966 (2955, 2956)			UNCLASSIFIED	1016
4840	79626143 (2969, 2970)			UNCLASSIFIED	1025, 1054
4841	66258467 (2991, 2992)			UNCLASSIFIED	1010
4842	65503433 (2995, 2996)			UNCLASSIFIED	1049
4843	9863838 (3009, 3010)			UNCLASSIFIED	1008
4844	65981228 (3025, 3026)			UNCLASSIFIED	1024
4845	8501919 (3075, 3076)			UNCLASSIFIED	1022
4846	78918087 (3091, 3092)			UNCLASSIFIED	1008, 1034
4847	91236209 (3095, 3096)			UNCLASSIFIED	1045
4848	27351119 (3113, 3114)			UNCLASSIFIED	1009
4849	13042410 (3125, 3126)			UNCLASSIFIED	1004
4850	80499456 (3133, 3134)			UNCLASSIFIED	1012
4851	78366834 (3137, 3138)			UNCLASSIFIED	1003
4852	79606217 (3141, 3142)			UNCLASSIFIED	1022, 1034
4853	80503986 (3143, 3144)			UNCLASSIFIED	1006, 1012
4854	9650539 (3171, 3172)			UNCLASSIFIED	1039
4855	10858672 (3193, 3194)			UNCLASSIFIED	1031
4856	79620177 (3197, 3198)			UNCLASSIFIED	1025

4857	27980198 (3231, 3232)			UNCLASSIFIED	1006
4858	65888269 (3237, 3238)			UNCLASSIFIED	1054
4859	94667164 (3261, 3262)			UNCLASSIFIED	1044
4860	65505812 (3265, 3266)			UNCLASSIFIED	1016
4861	78377906 (3267, 3268)			UNCLASSIFIED	1039
4862	28358655 (3279, 3280)			UNCLASSIFIED	1030, 1054
4863	94329389 (3287, 3288)			UNCLASSIFIED	1010
4864	85532538 (3289, 3290)			UNCLASSIFIED	1038
4865	10200245 (3299, 3300)			UNCLASSIFIED	1006
4866	13521875 (3301, 3302)			UNCLASSIFIED	1034
4867	29353200 (3309, 3310)			UNCLASSIFIED	1009
4868	33184749 (3311, 3312)			UNCLASSIFIED	1026
4869	21660695 (3321, 3322)			UNCLASSIFIED	1017, 1024
4870	79484179 (3327, 3328)			UNCLASSIFIED	1031
4871	80027391 (3337, 3338)			UNCLASSIFIED	1003, 1006, 1032
4872	11072274 (3353, 3354)			UNCLASSIFIED	1034
4873	36854820 (3363, 3364)			UNCLASSIFIED	1054
4874	95004965 (3365, 3366)			UNCLASSIFIED	1006, 1017, 1034

4875	78376978 (3381, 3382)			UNCLASSIFIED	1008
4876	11102092 (3383, 3384)			UNCLASSIFIED	1053
4877	20596518 (3407, 3408)			UNCLASSIFIED	1053
4878	57439464 (3413, 3414)			UNCLASSIFIED	1058
4879	79461401 (3417, 3418)			UNCLASSIFIED	1034
4880	78299175 (3423, 3424)			UNCLASSIFIED	1026
4881	23296404 (3429, 3430)			UNCLASSIFIED	1023
4882	78903906 (3433, 3434)			UNCLASSIFIED	1044
4883	23298372 (3437, 3438)			UNCLASSIFIED	1003, 1016, 1023, 1024, 1039
4884	19741635 (3445, 3446)			UNCLASSIFIED	1003
4885	95011723 (3481, 3482)			UNCLASSIFIED	1006
4886	33188621 (3497, 3498)			UNCLASSIFIED	1026
4887	29359063 (3505, 3506)			UNCLASSIFIED	1022
4888	94319574 (3529, 3530)			UNCLASSIFIED	1010
4889	37031442 (3533, 3534)			UNCLASSIFIED	1038
4890	35992049 (3535, 3536)			UNCLASSIFIED	1030
4891	20730668 (3545, 3546)			UNCLASSIFIED	1006
4892	80079949 (3563, 3564)			UNCLASSIFIED	1034

4893	16321749 (3587, 3588)			UNCLASSIFIED	1004
4894	65706307 (3593, 3594)			UNCLASSIFIED	1038
4895	80082839 (3597, 3598)			UNCLASSIFIED	1001
4896	28817494 (3611, 3612)			UNCLASSIFIED	1017
4897	94139733 (3617, 3618)			UNCLASSIFIED	1044
4898	70566738 (3629, 3630)			UNCLASSIFIED	1036
4899	18589178 (3643, 3644)			UNCLASSIFIED	1001
4900	79460967 (3649, 3650)			UNCLASSIFIED	1001
4901	33207465 (3653, 3654)			UNCLASSIFIED	1026
4902	56156638 (3671, 3672)			UNCLASSIFIED	1008
4903	12817719 (3673, 3674)			UNCLASSIFIED	1004
4904	23299970 (3675, 3676)			UNCLASSIFIED	1026
4905	20289286 (3689, 3690)			UNCLASSIFIED	1010
4906	79623244 (3695, 3696)			UNCLASSIFIED	1025
4907	80416739 (3697, 3698)			UNCLASSIFIED	1001, 1006, 1010, 1025
4908	37801561 (3711, 3712)			UNCLASSIFIED	1012
4909	80503340 (3715, 3716)			UNCLASSIFIED	1003, 1012, 1022, 1034, 1039, 1044, 1058
4910	23293220 (3723, 3724)			UNCLASSIFIED	1026

4911	20625040 (3755, 3756)			UNCLASSIFIED	1010
4912	66256637 (3757, 3758)			UNCLASSIFIED	1016
4913	33763794 (3761, 3762)			UNCLASSIFIED	1026
4914	65871999 (3771, 3772)			UNCLASSIFIED	1016
4915	35063178 (3781, 3782)			UNCLASSIFIED	1050
4916	78460774 (3791, 3792)			UNCLASSIFIED	1023
4917	38068620 (3829, 3830)			UNCLASSIFIED	1009
4918	29443084 (3831, 3832)			UNCLASSIFIED	1022
4919	95092187 (3843, 3844)			UNCLASSIFIED	1058
4920	95287608 (3847, 3848)			UNCLASSIFIED	1038
4921	18588229 (3849, 3850)			UNCLASSIFIED	1001
4922	95295881 (3853, 3854)			UNCLASSIFIED	1001, 1006, 1016, 1022, 1031, 1034, 1054
4923	80424759 (3859, 3860)			UNCLASSIFIED	1017, 1025
4924	7530006 (3861, 3862)			UNCLASSIFIED	1058
4925	77667713 (3869, 3870)			UNCLASSIFIED	1024
4926	34386848 (3883, 3884)			UNCLASSIFIED	1026
4927	80503349 (3885, 3886)			UNCLASSIFIED	1012
4928	56149706 (3887, 3888)			UNCLASSIFIED	1003

4929	32125815 (3891, 3892)			UNCLASSIFIED	1006
4930	56152322 (3907, 3908)			UNCLASSIFIED	1003
4931	20293364 (3925, 3926)			UNCLASSIFIED	1034
4932	56158098 (3929, 3930)			UNCLASSIFIED	1046
4933	78723348 (3943, 3944)			UNCLASSIFIED	1022, 1026
4934	91010277 (3955, 3956)			UNCLASSIFIED	1020
4935	85547145 (3959, 3960)			UNCLASSIFIED	1053
4936	79563081 (3963, 3964)			UNCLASSIFIED	1001
4937	65658407 (3969, 3970)			UNCLASSIFIED	1054
4938	79433671 (4011, 4012)			UNCLASSIFIED	1017
4939	65888332 (4015, 4016)			UNCLASSIFIED	1054
4940	36920987 (4019, 4020)			UNCLASSIFIED	1026
4941	32442464 (4065, 4066)			UNCLASSIFIED	1000
4942	65977620 (4075, 4076)			UNCLASSIFIED	1054
4943	87899145 (4085, 4086)			UNCLASSIFIED	1015
4944	55182619 (4087, 4088)			UNCLASSIFIED	1019
4945	95089890 (4093, 4094)			UNCLASSIFIED	1044
4946	10092799 (4127, 4128)			UNCLASSIFIED	1017

4947	15023937 (4135, 4136)			UNCLASSIFIED	1024
4948	39708546 (4153, 4154)			UNCLASSIFIED	1039
4949	20724562 (4157, 4158)			UNCLASSIFIED	1006
4950	79167066 (4177, 4178)			UNCLASSIFIED	1031
4951	16284579 (4183, 4184)			UNCLASSIFIED	1054
4952	54994274 (4185, 4186)			UNCLASSIFIED	1029
4953	80205103 (4191, 4192)			UNCLASSIFIED	1010, 1024, 1034
4954	20434401 (4201, 4202)			UNCLASSIFIED	1004
4955	9533119 (4209, 4210)			UNCLASSIFIED	1003
4956	13523038 (4229, 4230)			UNCLASSIFIED	1034
4957	94232306 (4231, 4232)			UNCLASSIFIED	1054
4958	20724566 (4237, 4238)			UNCLASSIFIED	1006
4959	65709209 (4239, 4240)			UNCLASSIFIED	1023
4960	87586834 (4245, 4246)			UNCLASSIFIED	1003
4961	77651477 (4265, 4266)			UNCLASSIFIED	1038
4962	11466067 (4269, 4270)			UNCLASSIFIED	1024
4963	99412985 (4273, 4274)			UNCLASSIFIED	1003, 1022, 1023, 1025
4964	27982079 (4277, 4278)			UNCLASSIFIED	1053

4965	52563623 (4293, 4294)			UNCLASSIFIED	1044
4966	19641476 (4307, 4308)			UNCLASSIFIED	1034
4967	78389955 (4313, 4314)			UNCLASSIFIED	1019, 1030, 1040, 1041
4968	80081684 (4315, 4316)			UNCLASSIFIED	1019, 1022, 1042, 1054
4969	80106006 (4319, 4320)			UNCLASSIFIED	1007
4970	79647505 (4327, 4328)			UNCLASSIFIED	1017, 1038
4971	9678256 (4329, 4330)			UNCLASSIFIED	1044
4972	32691420 (4339, 4340)			UNCLASSIFIED	1029
4973	79861716 (4345, 4346)			UNCLASSIFIED	1023, 1024, 1044
4974	29345933 (4355, 4356)			UNCLASSIFIED	1022
4975	78269395 (4359, 4360)			UNCLASSIFIED	1029
4976	20297622 (4373, 4374)			UNCLASSIFIED	1034
4977	79631893 (4377, 4378)			UNCLASSIFIED	1034
4978	65476799 (4379, 4380)			UNCLASSIFIED	1038
4979	39550317 (4383, 4384)			UNCLASSIFIED	1039
4980	30521361 (4391, 4392)			UNCLASSIFIED	1054
4981	5280402 (4421, 4422)			UNCLASSIFIED	1058
4982	65696966 (4423, 4424)			UNCLASSIFIED	1038

4983	78790727 (4463, 4464)			UNCLASSIFIED	1044
4984	57311075 (4477, 4478)			UNCLASSIFIED	1054
4985	80591913 (4481, 4482)			UNCLASSIFIED	1026, 1034, 1058
4986	21426530 (4489, 4490)			UNCLASSIFIED	1022
4987	9860417 (4491, 4492)			UNCLASSIFIED	1008
4988	78407047 (4499, 4500)			UNCLASSIFIED	1024
4989	19518039 (4503, 4504)			UNCLASSIFIED	1003
4990	19894316 (4511, 4512)			UNCLASSIFIED	1022
4991	47652936 (4529, 4530)			UNCLASSIFIED	1029
4992	80025810 (4535, 4536)			UNCLASSIFIED	1006
4993	80092973 (4537, 4538)			UNCLASSIFIED	1006
4994	79889279 (4553, 4554)			UNCLASSIFIED	1017
4995	65674254 (4559, 4560)			UNCLASSIFIED	1016
4996	20632651 (4567, 4568)			UNCLASSIFIED	1024
4997	80384201 (4569, 4570)			UNCLASSIFIED	1029, 1050
4998	11130417 (4603, 4604)			UNCLASSIFIED	1034
4999	20731631 (4613, 4614)			UNCLASSIFIED	1006
5000	54857231 (4615, 4616)			UNCLASSIFIED	1019

5001	91235214 (4641, 4642)			UNCLASSIFIED	1010
5002	29470614 (4645, 4646)			UNCLASSIFIED	1026
5003	20378287 (4649, 4650)			UNCLASSIFIED	1004
5004	65874179 (4655, 4656)			UNCLASSIFIED	1003, 1016
5005	20216800 (4673, 4674)			UNCLASSIFIED	1004
5006	11810888 (4681, 4682)			UNCLASSIFIED	1022
5007	79963471 (4691, 4692)			UNCLASSIFIED	1016, 1038, 1044
5008	29690930 (4699, 4700)			UNCLASSIFIED	1024
5009	94137625 (4705, 4706)			UNCLASSIFIED	1044
5010	78270787 (4707, 4708)			UNCLASSIFIED	1039
5011	78506918 (4719, 4720)			UNCLASSIFIED	1030, 1054
5012	78730258 (4733, 4734)			UNCLASSIFIED	1023
5013	66138179 (4737, 4738)			UNCLASSIFIED	1003, 1024
5014	77664712 (4745, 4746)			UNCLASSIFIED	1022
5015	91232572 (4759, 4760)			UNCLASSIFIED	1002, 1010, 1024
5016	78056504 (4761, 4762)			UNCLASSIFIED	1037
5017	25250283 (4779, 4780)			UNCLASSIFIED	1039
5018	71095657 (4787, 4788)			UNCLASSIFIED	1029, 1053

5019	80020416 (4799, 4800)			UNCLASSIFIED	1053
5020	79860962 (4803, 4804)			UNCLASSIFIED	1024, 1038, 1054
5021	28976415 (4813, 4814)			UNCLASSIFIED	1022
5022	66726532 (4815, 4816)			UNCLASSIFIED	1009
5023	16801293 (4819, 4820)			UNCLASSIFIED	1017
5024	27826607 (4827, 4828)			UNCLASSIFIED	1022
5025	66142961 (4831, 4832)			UNCLASSIFIED	1010
5026	11805813 (4833, 4834)			UNCLASSIFIED	1022
5027	19755176 (4841, 4842)			UNCLASSIFIED	1003
5028	80468746 (4847, 4848)			UNCLASSIFIED	1012
5029	78793921 (4853, 4854)			UNCLASSIFIED	1003
5030	78510515 (4869, 4870)			UNCLASSIFIED	1008
5031	30274244 (4873, 4874)			UNCLASSIFIED	1008
5032	38057378 (4879, 4880)			UNCLASSIFIED	1054
5033	78928871 (4891, 4892)			UNCLASSIFIED	1039
5034	78380066 (4897, 4898)			UNCLASSIFIED	1008
5035	36858272 (4911, 4912)			UNCLASSIFIED	1016
5036	29225344 (4913, 4914)			UNCLASSIFIED	1024, 1026

5037	90939146 (4919, 4920)			UNCLASSIFIED	1020, 1046
5038	80499622 (4923, 4924)			UNCLASSIFIED	1003, 1012, 1017, 1034, 1038, 1039
5039	65481477 (4925, 4926)			UNCLASSIFIED	1001, 1049
5040	57307997 (4935, 4936)			UNCLASSIFIED	1022
5041	39734786 (4943, 4944)			UNCLASSIFIED	1026
5042	9948059 (4953, 4954)			UNCLASSIFIED	1044
5043	86667240 (4957, 4958)			UNCLASSIFIED	1029
5044	78797184 (4965, 4966)			UNCLASSIFIED	1026
5045	11310927 (4983, 4984)			UNCLASSIFIED	1024
5046	65652928 (4987, 4988)			UNCLASSIFIED	1016
5047	78254988 (4989, 4990)			UNCLASSIFIED	1010, 1016, 1058
5048	17898109 (4997, 4998)			UNCLASSIFIED	1044
5049	9287013 (5003, 5004)			UNCLASSIFIED	1008
5050	78769680 (5029, 5030)			UNCLASSIFIED	1022
5051	36507186 (5035, 5036)			UNCLASSIFIED	1026
5052	25134632 (5037, 5038)			UNCLASSIFIED	1003
5053	52471815 (5041, 5042)			UNCLASSIFIED	1036
5054	20289034 (5051, 5052)			UNCLASSIFIED	1034

5055	20475851 (5063, 5064)			UNCLASSIFIED	1022
5056	14995783 (5065, 5066)			UNCLASSIFIED	1024
5057	6343085 (5073, 5074)			UNCLASSIFIED	1058
5058	25264663 (5077, 5078)			UNCLASSIFIED	1054
5059	27957182 (5081, 5082)			UNCLASSIFIED	1004, 1010, 1024
5060	66396658 (5091, 5092)			UNCLASSIFIED	1008
5061	79399274 (5103, 5104)			UNCLASSIFIED	1024
5062	91230076 (5111, 5112)			UNCLASSIFIED	1020, 1054
5063	20297053 (5147, 5148)			UNCLASSIFIED	1022
5064	29692275 (5155, 5156)			UNCLASSIFIED	1016
5065	20688080 (5157, 5158)			UNCLASSIFIED	1010, 1024
5066	16300448 (5159, 5160)			UNCLASSIFIED	1054
5067	36903066 (5177, 5178)			UNCLASSIFIED	1026
5068	29142136 (5221, 5222)			UNCLASSIFIED	1017
5069	79757861 (5227, 5228)			UNCLASSIFIED	1008
5070	32116280 (5229, 5230)			UNCLASSIFIED	1026
5071	20148258 (5235, 5236)			UNCLASSIFIED	1010
5072	47652772 (5237, 5238)			UNCLASSIFIED	1029

5073	38923105 (5245, 5246)			UNCLASSIFIED	1008
5074	80408722 (5253, 5254)			UNCLASSIFIED	1003, 1004, 1006, 1008, 1016, 1017, 1023, 1024, 1025, 1029, 1034, 1038, 1039, 1044, 1054
5075	20753937 (5275, 5276)			UNCLASSIFIED	1006
5076	65485023 (5291, 5292)			UNCLASSIFIED	1009
5077	14973283 (5321, 5322)			UNCLASSIFIED	1024
5078	11750358 (5337, 5338)			UNCLASSIFIED	1038
5079	80238539 (5339, 5340)			UNCLASSIFIED	1009, 1022, 1024
5080	20432749 (5347, 5348)			UNCLASSIFIED	1024
5081	15021978 (5361, 5362)			UNCLASSIFIED	1001
5082	21416541 (5373, 5374)			UNCLASSIFIED	1022
5083	79841764 (5395, 5396)			UNCLASSIFIED	1044
5084	79560547 (5405, 5406)			UNCLASSIFIED	1001
5085	80056227 (5409, 5410)			UNCLASSIFIED	1022
5086	15034786 (5423, 5424)			UNCLASSIFIED	1004
5087	27982168 (5425, 5426)			UNCLASSIFIED	1006
5088	27829707 (5437, 5438)			UNCLASSIFIED	1010, 1022, 1024, 1034

5089	9859112 (5453, 5454)			UNCLASSIFIED	1008
5090	85524525 (5459, 5460)			UNCLASSIFIED	1038
5091	25147891 (5487, 5488)			UNCLASSIFIED	1026
5092	80079956 (5495, 5496)			UNCLASSIFIED	1034
5093	36840157 (5505, 5506)			UNCLASSIFIED	1054
5094	46895245 (5511, 5512)			UNCLASSIFIED	1040
5095	32275643 (5529, 5530)			UNCLASSIFIED	1029
5096	79852247 (5531, 5532)			UNCLASSIFIED	1017
5097	8488502 (5533, 5534)			UNCLASSIFIED	1024
5098	28996372 (5555, 5556)			UNCLASSIFIED	1008
5099	80582192 (5561, 5562)			UNCLASSIFIED	1003, 1010, 1039
5100	55184282 (5577, 5578)			UNCLASSIFIED	1019
5101	10095562 (5579, 5580)			UNCLASSIFIED	1025
5102	16843283 (5587, 5588)			UNCLASSIFIED	1039
5103	11765993 (5593, 5594)			UNCLASSIFIED	1025
5104	65986561 (5605, 5606)			UNCLASSIFIED	1054
5105	94235040 (5609, 5610)			UNCLASSIFIED	1054
5106	79877515 (5615, 5616)			UNCLASSIFIED	1012, 1034

5107	71238348 (5633, 5634)			UNCLASSIFIED	1000, 1019
5108	79475917 (5635, 5636)			UNCLASSIFIED	1038
5109	32155939 (5657, 5658)			UNCLASSIFIED	1044
5110	78254622 (5683, 5684)			UNCLASSIFIED	1026
5111	16499916 (5687, 5688)			UNCLASSIFIED	1030
5112	54699268 (5693, 5694)			UNCLASSIFIED	1041
5113	79854084 (5695, 5696)			UNCLASSIFIED	1008, 1044
5114	78753175 (5709, 5710)			UNCLASSIFIED	1003, 1017, 1023, 1039, 1044
5115	79190323 (5715, 5716)			UNCLASSIFIED	1024
5116	80245767 (5727, 5728)			UNCLASSIFIED	1004, 1006, 1010, 1012, 1017, 1022, 1034
5117	11688860 (5737, 5738)			UNCLASSIFIED	1031
5118	29357248 (5763, 5764)			UNCLASSIFIED	1026
5119	78908616 (5765, 5766)			UNCLASSIFIED	1023, 1039
5120	66397455 (5767, 5768)			UNCLASSIFIED	1008
5121	80385633 (5781, 5782)			UNCLASSIFIED	1029
5122	86477086 (5809, 5810)			UNCLASSIFIED	1029
5123	86470542 (5829, 5830)			UNCLASSIFIED	1019, 1026
5124	10343959 (5831, 5832)			UNCLASSIFIED	1038

5125	80496485 (5835, 5836)			UNCLASSIFIED	1012
5126	13084299 (5839, 5840)			UNCLASSIFIED	1024
5127	66436551 (5853, 5854)			UNCLASSIFIED	1024, 1050
5128	27835807 (5859, 5860)			UNCLASSIFIED	1010, 1024, 1034
5129	30268690 (5863, 5864)			UNCLASSIFIED	1044
5130	78303488 (5875, 5876)			UNCLASSIFIED	1026
5131	79213573 (5893, 5894)			UNCLASSIFIED	1040, 1054
5132	19847679 (5925, 5926)			UNCLASSIFIED	1034
5133	79562917 (5927, 5928)			UNCLASSIFIED	1001
5134	29515957 (5929, 5930)			UNCLASSIFIED	1026
5135	82309349 (5931, 5932)			UNCLASSIFIED	1001
5136	29005829 (5939, 5940)			UNCLASSIFIED	1017
5137	79316662 (5959, 5960)			UNCLASSIFIED	1053
5138	77802701 (5963, 5964)			UNCLASSIFIED	1054
5139	91014633 (5971, 5972)			UNCLASSIFIED	1010
5140	29691078 (5977, 5978)			UNCLASSIFIED	1001, 1024
5141	20291572 (6005, 6006)			UNCLASSIFIED	1022
5142	79157906 (6013, 6014)			UNCLASSIFIED	1006

5143	79558070 (6015, 6016)			UNCLASSIFIED	1003
5144	32304160 (6021, 6022)			UNCLASSIFIED	1000
5145	30645675 (6023, 6024)			UNCLASSIFIED	1008
5146	86466972 (6025, 6026)			UNCLASSIFIED	1029
5147	28459869 (6029, 6030)			UNCLASSIFIED	1030
5148	57058597 (6031, 6032)			UNCLASSIFIED	1054
5149	10262117 (6037, 6038)			UNCLASSIFIED	1023
5150	95416994 (6039, 6040)			UNCLASSIFIED	1017, 1029, 1058
5151	78029109 (6043, 6044)			UNCLASSIFIED	1026
5152	79635269 (6055, 6056)			UNCLASSIFIED	1038
5153	16930411 (6061, 6062)			UNCLASSIFIED	1039
5154	55187264 (6069, 6070)			UNCLASSIFIED	1019
5155	10358054 (6073, 6074)			UNCLASSIFIED	1039
5156	78392326 (6077, 6078)			UNCLASSIFIED	1030, 1034
5157	49826371 (6083, 6084)			UNCLASSIFIED	1036
5158	37798845 (6107, 6108)			UNCLASSIFIED	1012
5159	17931705 (6123, 6124)			UNCLASSIFIED	1023
5160	8502281 (6129, 6130)			UNCLASSIFIED	1010

5161	11799333 (6141, 6142)			UNCLASSIFIED	1038
5162	79637416 (6147, 6148)			UNCLASSIFIED	1044
5163	79581619 (6151, 6152)			UNCLASSIFIED	1016, 1040
5164	52229898 (6155, 6156)			UNCLASSIFIED	1036
5165	79796272 (6157, 6158)			UNCLASSIFIED	1024, 1025, 1044
5166	30537150 (6173, 6174)			UNCLASSIFIED	1026
5167	78523718 (6175, 6176)			UNCLASSIFIED	1008
5168	88068474 (6177, 6178)			UNCLASSIFIED	1053
5169	11130780 (6185, 6186)			UNCLASSIFIED	1006
5170	16421170 (6189, 6190)			UNCLASSIFIED	1003
5171	20633758 (6193, 6194)			UNCLASSIFIED	1004
5172	79846212 (6211, 6212)			UNCLASSIFIED	1044
5173	28374356 (6213, 6214)			UNCLASSIFIED	1024
5174	98943853 (6215, 6216)			UNCLASSIFIED	1010, 1031, 1043
5175	25248469 (6221, 6222)			UNCLASSIFIED	1023
5176	80039970 (6225, 6226)			UNCLASSIFIED	1022
5177	79610204 (6227, 6228)			UNCLASSIFIED	1039
5178	57057121 (6237, 6238)			UNCLASSIFIED	1054

5179	86465890 (6239, 6240)			UNCLASSIFIED	1029
5180	20294907 (6243, 6244)			UNCLASSIFIED	1022
5181	80085241 (6245, 6246)			UNCLASSIFIED	1054
5182	87455587 (6255, 6256)			UNCLASSIFIED	1025
5183	78971204 (6265, 6266)			UNCLASSIFIED	1003
5184	27805779 (6271, 6272)			UNCLASSIFIED	1022
5185	47652261 (6281, 6282)			UNCLASSIFIED	1029
5186	91228201 (6289, 6290)			UNCLASSIFIED	1010
5187	21437311 (6297, 6298)			UNCLASSIFIED	1034
5188	37034503 (6299, 6300)			UNCLASSIFIED	1012
5189	79914983 (6309, 6310)			UNCLASSIFIED	1044
5190	10279756 (6311, 6312)			UNCLASSIFIED	1025
5191	78379792 (6317, 6318)			UNCLASSIFIED	1026
5192	37017019 (6333, 6334)			UNCLASSIFIED	1025
5193	79815629 (6341, 6342)			UNCLASSIFIED	1017, 1039
5194	86379956 (6353, 6354)			UNCLASSIFIED	1053
5195	19479854 (6359, 6360)			UNCLASSIFIED	1038
5196	79587630 (6369, 6370)			UNCLASSIFIED	1006

5197	49297665 (6379, 6380)			UNCLASSIFIED	1036
5198	20465261 (6387, 6388)			UNCLASSIFIED	1010
5199	17663280 (6393, 6394)			UNCLASSIFIED	1025
5200	20459354 (6403, 6404)			UNCLASSIFIED	1006
5201	37011661 (6415, 6416)			UNCLASSIFIED	1029
5202	79485207 (6435, 6436)			UNCLASSIFIED	1034
5203	78206913 (6455, 6456)			UNCLASSIFIED	1054
5204	65881670 (6481, 6482)			UNCLASSIFIED	1054
5205	71758071 (6495, 6496)			UNCLASSIFIED	1017, 1023
5206	20431621 (6511, 6512)			UNCLASSIFIED	1010
5207	80407779 (6513, 6514)			UNCLASSIFIED	1029
5208	49128786 (6519, 6520)			UNCLASSIFIED	1040
5209	11071847 (6525, 6526)			UNCLASSIFIED	1034
5210	78947573 (6527, 6528)			UNCLASSIFIED	1017
5211	65691882 (6541, 6542)			UNCLASSIFIED	1009
5212	12806274 (6565, 6566)			UNCLASSIFIED	1004
5213	80186759 (6575, 6576)			UNCLASSIFIED	1058
5214	77978838 (6581, 6582)			UNCLASSIFIED	1024, 1036

5215	65686186 (6587, 6588)			UNCLASSIFIED	1024
5216	25317501 (6597, 6598)			UNCLASSIFIED	1009
5217	29353222 (6601, 6602)			UNCLASSIFIED	1017
5218	65669283 (6623, 6624)			UNCLASSIFIED	1016
5219	80025952 (6629, 6630)			UNCLASSIFIED	1006, 1023, 1024
5220	78985627 (6631, 6632)			UNCLASSIFIED	1054
5221	28348543 (6645, 6646)			UNCLASSIFIED	1024
5222	20466053 (6665, 6666)			UNCLASSIFIED	1010
5223	86686787 (6673, 6674)			UNCLASSIFIED	1013
5224	81618962 (6691, 6692)			UNCLASSIFIED	1004, 1029, 1053, 1054
5225	71770376 (6733, 6734)			UNCLASSIFIED	1003
5226	94317606 (6739, 6740)			UNCLASSIFIED	1044
5227	71811056 (6741, 6742)			UNCLASSIFIED	1022, 1054
5228	54860772 (6751, 6752)			UNCLASSIFIED	1019
5229	16844173 (6757, 6758)			UNCLASSIFIED	1039
5230	97993351 (6759, 6760)			UNCLASSIFIED	1003, 1008, 1010, 1017, 1023, 1024, 1025, 1029, 1038, 1044, 1054
5231	79921799 (6769, 6770)			UNCLASSIFIED	1003

5232	87459284 (6779, 6780)			UNCLASSIFIED	1019, 1023, 1025
5233	80259500 (6785, 6786)			UNCLASSIFIED	1024
5234	66176310 (6795, 6796)			UNCLASSIFIED	1016
5235	79957388 (6821, 6822)			UNCLASSIFIED	1025
5236	19879311 (6831, 6832)			UNCLASSIFIED	1022
5237	65703727 (6843, 6844)			UNCLASSIFIED	1038
5238	6329184 (6845, 6846)			UNCLASSIFIED	1058
5239	35091694 (6853, 6854)			UNCLASSIFIED	1050
5240	79974494 (6869, 6870)			UNCLASSIFIED	1025
5241	86380275 (6873, 6874)			UNCLASSIFIED	1053
5242	80420196 (6881, 6882)			UNCLASSIFIED	1008, 1016, 1017, 1025, 1054
5243	40389445 (6885, 6886)			UNCLASSIFIED	1037
5244	37032328 (6889, 6890)			UNCLASSIFIED	1038
5245	3371936 (6893, 6894)			UNCLASSIFIED	1012
5246	11415729 (6897, 6898)			UNCLASSIFIED	1017
5247	27241770 (6899, 6900)			UNCLASSIFIED	1023
5248	80084606 (6901, 6902)			UNCLASSIFIED	1001, 1034
5249	10328610 (6927, 6928)			UNCLASSIFIED	1025

5250	78951028 (6935, 6936)			UNCLASSIFIED	1023, 1054
5251	80090969 (6965, 6966)			UNCLASSIFIED	1049, 1054
5252	47656639 (6969, 6970)			UNCLASSIFIED	1029
5253	78387151 (6971, 6972)			UNCLASSIFIED	1009, 1044
5254	77673816 (6977, 6978)			UNCLASSIFIED	1003
5255	20630336 (6981, 6982)			UNCLASSIFIED	1004
5256	79671979 (6995, 6996)			UNCLASSIFIED	1010, 1017
5257	25139076 (7005, 7006)			UNCLASSIFIED	1003
5258	79446849 (7015, 7016)			UNCLASSIFIED	1022
5259	13076280 (7031, 7032)			UNCLASSIFIED	1027
5260	66037340 (7033, 7034)			UNCLASSIFIED	1021, 1029, 1032, 1035, 1041, 1054
5261	20295126 (7035, 7036)			UNCLASSIFIED	1034
5262	78184009 (7059, 7060)			UNCLASSIFIED	1053
5263	79211075 (7065, 7066)			UNCLASSIFIED	1054
5264	11306931 (7067, 7068)			UNCLASSIFIED	1022
5265	80049785 (7071, 7072)			UNCLASSIFIED	1008, 1023, 1034, 1039
5266	97993359 (7077, 7078)			UNCLASSIFIED	1010, 1017, 1044, 1054
5267	55762455 (7085, 7086)			UNCLASSIFIED	1044

5268	78052078 (7093, 7094)			UNCLASSIFIED	1026
5269	88003828 (7095, 7096)			UNCLASSIFIED	1053
5270	9882665 (7105, 7106)			UNCLASSIFIED	1008
5271	10887321 (7137, 7138)			UNCLASSIFIED	1027
5272	11816423 (7145, 7146)			UNCLASSIFIED	1004
5273	56516535 (7149, 7150)			UNCLASSIFIED	1019
5274	78297732 (7151, 7152)			UNCLASSIFIED	1026
5275	27832512 (7169, 7170)			UNCLASSIFIED	1022
5276	79178341 (7185, 7186)			UNCLASSIFIED	1027
5277	55166988 (7203, 7204)			UNCLASSIFIED	1050
5278	30539340 (7207, 7208)			UNCLASSIFIED	1026
5279	82046666 (7237, 7238)			UNCLASSIFIED	1004, 1006, 1010, 1016, 1017, 1022, 1024, 1034
5280	37402588 (7245, 7246)			UNCLASSIFIED	1022
5281	66255585 (7249, 7250)			UNCLASSIFIED	1016
5282	46845180 (7263, 7264)			UNCLASSIFIED	1029
5283	16287283 (7265, 7266)			UNCLASSIFIED	1024
5284	79915038 (7267, 7268)			UNCLASSIFIED	1017

5285	77582744 (7273, 7274)			UNCLASSIFIED	1008
5286	55862230 (7281, 7282)			UNCLASSIFIED	1038
5287	65696312 (7283, 7284)			UNCLASSIFIED	1038
5288	38439731 (7287, 7288)			UNCLASSIFIED	1054
5289	79480190 (7289, 7290)			UNCLASSIFIED	1016
5290	30635858 (7309, 7310)			UNCLASSIFIED	1026
5291	78676478 (7319, 7320)			UNCLASSIFIED	1026
5292	94845520 (7337, 7338)			UNCLASSIFIED	1023, 1044
5293	78466294 (7359, 7360)			UNCLASSIFIED	1026
5294	29343577 (7369, 7370)			UNCLASSIFIED	1044
5295	21415303 (7373, 7374)			UNCLASSIFIED	1034
5296	25337090 (7375, 7376)			UNCLASSIFIED	1008
5297	79842689 (7409, 7410)			UNCLASSIFIED	1008
5298	65981076 (7423, 7424)			UNCLASSIFIED	1024
5299	80020956 (7431, 7432)			UNCLASSIFIED	1022
5300	9893852 (7437, 7438)			UNCLASSIFIED	1039
5301	27981587 (7439, 7440)			UNCLASSIFIED	1006
5302	80232031 (7453, 7454)			UNCLASSIFIED	1010, 1022, 1034

5303	80478229 (7455, 7456)			UNCLASSIFIED	1012
5304	27958113 (7467, 7468)			UNCLASSIFIED	1022
5305	10801357 (7471, 7472)			UNCLASSIFIED	1017
5306	79832873 (7477, 7478)			UNCLASSIFIED	1023
5307	30198354 (7495, 7496)			UNCLASSIFIED	1026
5308	17888313 (7497, 7498)			UNCLASSIFIED	1023
5309	25256495 (7505, 7506)			UNCLASSIFIED	1026
5310	54540267 (7521, 7522)			UNCLASSIFIED	1041
5311	20287238 (7551, 7552)			UNCLASSIFIED	1034
5312	80502619 (7553, 7554)			UNCLASSIFIED	1004, 1006, 1010, 1012, 1022, 1024, 1027, 1031, 1034
5313	28389124 (7565, 7566)			UNCLASSIFIED	1054
5314	27845382 (7567, 7568)			UNCLASSIFIED	1022
5315	66390306 (7571, 7572)			UNCLASSIFIED	1004, 1006, 1038
5316	7529965 (7575, 7576)			UNCLASSIFIED	1058
5317	65881563 (7577, 7578)			UNCLASSIFIED	1016
5318	54894326 (7609, 7610)			UNCLASSIFIED	1041
5319	11358001 (7631, 7632)			UNCLASSIFIED	1058

5320	32742508 (7653, 7654)			UNCLASSIFIED	1012
5321	11769418 (7659, 7660)			UNCLASSIFIED	1027
5322	86381109 (7665, 7666)			UNCLASSIFIED	1053
5323	79633483 (7669, 7670)			UNCLASSIFIED	1016, 1038
5324	85512909 (7675, 7676)			UNCLASSIFIED	1053
5325	78771376 (7685, 7686)			UNCLASSIFIED	1039
5326	78317247 (7691, 7692)			UNCLASSIFIED	1026
5327	11362141 (7695, 7696)			UNCLASSIFIED	1024
5328	94672870 (7699, 7700)			UNCLASSIFIED	1031, 1034
5329	32739119 (7701, 7702)			UNCLASSIFIED	1012
5330	17897290 (7715, 7716)			UNCLASSIFIED	1024
5331	21433383 (7717, 7718)			UNCLASSIFIED	1022, 1024
5332	65462322 (7719, 7720)			UNCLASSIFIED	1054
5333	78373342 (7721, 7722)			UNCLASSIFIED	1013
5334	80199079 (7725, 7726)			UNCLASSIFIED	1034
5335	80041749 (7731, 7732)			UNCLASSIFIED	1022
5336	87454729 (7737, 7738)			UNCLASSIFIED	1025
5337	94129384 (7743, 7744)			UNCLASSIFIED	1025

5338	47656514 (7745, 7746)			UNCLASSIFIED	1029, 1053
5339	80078875 (7749, 7750)			UNCLASSIFIED	1001, 1023, 1034, 1054
5340	66173240 (7753, 7754)			UNCLASSIFIED	1016
5341	36831091 (7761, 7762)			UNCLASSIFIED	1054
5342	30173985 (7767, 7768)			UNCLASSIFIED	1016
5343	78781003 (7769, 7770)			UNCLASSIFIED	1026
5344	80451553 (7783, 7784)			UNCLASSIFIED	1017, 1038, 1044
5345	20435513 (7785, 7786)			UNCLASSIFIED	1024
5346	47652570 (7797, 7798)			UNCLASSIFIED	1029
5347	35058689 (7799, 7800)			UNCLASSIFIED	1050
5348	15028582 (7805, 7806)			UNCLASSIFIED	1054
5349	13085170 (7841, 7842)			UNCLASSIFIED	1024
5350	11307308 (7869, 7870)			UNCLASSIFIED	1024
5351	65495369 (7873, 7874)			UNCLASSIFIED	1023
5352	65885027 (7911, 7912)			UNCLASSIFIED	1054
5353	10194093 (7919, 7920)			UNCLASSIFIED	1003
5354	19858661 (7937, 7938)			UNCLASSIFIED	1034
5355	79233133 (7939, 7940)			UNCLASSIFIED	1001

5356	80034646 (7941, 7942)			UNCLASSIFIED	1053
5357	25259664 (7975, 7976)			UNCLASSIFIED	1008
5358	77884135 (7981, 7982)			UNCLASSIFIED	1021
5359	79193832 (7985, 7986)			UNCLASSIFIED	1024
5360	80051547 (7987, 7988)			UNCLASSIFIED	1004
5361	35606174 (8007, 8008)			UNCLASSIFIED	1053
5362	80200441 (8017, 8018)			UNCLASSIFIED	1034
5363	79776383 (8019, 8020)			UNCLASSIFIED	1003
5364	33201958 (8031, 8032)			UNCLASSIFIED	1026
5365	34270252 (8045, 8046)			UNCLASSIFIED	1028
5366	77918724 (8051, 8052)			UNCLASSIFIED	1036
5367	65497348 (8057, 8058)			UNCLASSIFIED	1016
5368	79249505 (8069, 8070)			UNCLASSIFIED	1003, 1038
5369	29676953 (8085, 8086)			UNCLASSIFIED	1030
5370	80503197 (8105, 8106)			UNCLASSIFIED	1004, 1012, 1034
5371	11602289 (8107, 8108)			UNCLASSIFIED	1024
5372	79261068 (8121, 8122)			UNCLASSIFIED	1024, 1054
5373	39500183 (8127, 8128)			UNCLASSIFIED	1006

5374	34408232 (8131, 8132)			UNCLASSIFIED	1030
5375	79474566 (8135, 8136)			UNCLASSIFIED	1025
5376	34408864 (8139, 8140)			UNCLASSIFIED	1026
5377	79574372 (8145, 8146)			UNCLASSIFIED	1010, 1023, 1031, 1049
5378	86670079 (8149, 8150)			UNCLASSIFIED	1054
5379	17290402 (8157, 8158)			UNCLASSIFIED	1008
5380	94315126 (8161, 8162)			UNCLASSIFIED	1020
5381	78707921 (8169, 8170)			UNCLASSIFIED	1008
5382	78911634 (8179, 8180)			UNCLASSIFIED	1017, 1037
5383	11765583 (8219, 8220)			UNCLASSIFIED	1038
5384	20467267 (8239, 8240)			UNCLASSIFIED	1010
5385	80100236 (8241, 8242)			UNCLASSIFIED	1004, 1016, 1026
5386	79330843 (8243, 8244)			UNCLASSIFIED	1022
5387	86689822 (8245, 8246)			UNCLASSIFIED	1022, 1023
5388	16521538 (8247, 8248)			UNCLASSIFIED	1003, 1034
5389	65897456 (8265, 8266)			UNCLASSIFIED	1006, 1016
5390	46849742 (8281, 8282)			UNCLASSIFIED	1029
5391	11102986 (8283, 8284)			UNCLASSIFIED	1053

5392	18545703 (8303, 8304)			UNCLASSIFIED	1058
5393	55309111 (8305, 8306)			UNCLASSIFIED	1019
5394	79834547 (8309, 8310)			UNCLASSIFIED	1008
5395	42723360 (8311, 8312)			UNCLASSIFIED	1000
5396	95002700 (8321, 8322)			UNCLASSIFIED	1003, 1022
5397	30536440 (8327, 8328)			UNCLASSIFIED	1026
5398	70336466 (8329, 8330)			UNCLASSIFIED	1034, 1049
5399	79635459 (8331, 8332)			UNCLASSIFIED	1008
5400	20595048 (8337, 8338)			UNCLASSIFIED	1034
5401	79872888 (8353, 8354)			UNCLASSIFIED	1034
5402	94991741 (8359, 8360)			UNCLASSIFIED	1004, 1006, 1039
5403	66123463 (8371, 8372)			UNCLASSIFIED	1003
5404	19507330 (8391, 8392)			UNCLASSIFIED	1044
5405	20287851 (8401, 8402)			UNCLASSIFIED	1034
5406	20565009 (8407, 8408)			UNCLASSIFIED	1058
5407	17933170 (8417, 8418)			UNCLASSIFIED	1008
5408	79617973 (8427, 8428)			UNCLASSIFIED	1004
5409	86377020 (8433, 8434)			UNCLASSIFIED	1000, 1006, 1016, 1024

5410	10194277 (8435, 8436)			UNCLASSIFIED	1001
5411	66363898 (8451, 8452)			UNCLASSIFIED	1004
5412	80574192 (8459, 8460)			UNCLASSIFIED	1003, 1058
5413	20478822 (8469, 8470)			UNCLASSIFIED	1022
5414	79191734 (8483, 8484)			UNCLASSIFIED	1034
5415	80035632 (8497, 8498)			UNCLASSIFIED	1010
5416	78928891 (8505, 8506)			UNCLASSIFIED	1017, 1023, 1039
5417	20720192 (8519, 8520)			UNCLASSIFIED	1053
5418	20616476 (8527, 8528)			UNCLASSIFIED	1022
5419	30388369 (8535, 8536)			UNCLASSIFIED	1038
5420	11686751 (8539, 8540)			UNCLASSIFIED	1031
5421	20466876 (8547, 8548)			UNCLASSIFIED	1010
5422	11809277 (8549, 8550)			UNCLASSIFIED	1038
5423	80427709 (8559, 8560)			UNCLASSIFIED	1024, 1025, 1044
5424	78522274 (8595, 8596)			UNCLASSIFIED	1044
5425	20438241 (8613, 8614)			UNCLASSIFIED	1010
5426	35896006 (8623, 8624)			UNCLASSIFIED	1053
5427	33764452 (8625, 8626)			UNCLASSIFIED	1026

5428	79907203 (8633, 8634)			UNCLASSIFIED	1022, 1038
5429	11809884 (8649, 8650)			UNCLASSIFIED	1016
5430	5980033 (8651, 8652)			UNCLASSIFIED	1058
5431	17707255 (8653, 8654)			UNCLASSIFIED	1008
5432	79564076 (8655, 8656)			UNCLASSIFIED	1017
5433	87452763 (8667, 8668)			UNCLASSIFIED	1008, 1025
5434	80025968 (8675, 8676)			UNCLASSIFIED	1001, 1006, 1017
5435	52493263 (8683, 8684)			UNCLASSIFIED	1036
5436	9398503 (8707, 8708)			UNCLASSIFIED	1017
5437	10299709 (8709, 8710)			UNCLASSIFIED	1038
5438	10868168 (8713, 8714)			UNCLASSIFIED	1034
5439	79872946 (8717, 8718)			UNCLASSIFIED	1001
5440	27842667 (8719, 8720)			UNCLASSIFIED	1004, 1024
5441	30662594 (8721, 8722)			UNCLASSIFIED	1026
5442	30789081 (8725, 8726)			UNCLASSIFIED	1026
5443	46895172 (8753, 8754)			UNCLASSIFIED	1019
5444	9875346 (8779, 8780)			UNCLASSIFIED	1044
5445	30386041 (8785, 8786)			UNCLASSIFIED	1016

5446	79778177 (8793, 8794)			UNCLASSIFIED	1017
5447	79110241 (8807, 8808)			UNCLASSIFIED	1025
5448	10106140 (8813, 8814)			UNCLASSIFIED	1017
5449	37815429 (8815, 8816)			UNCLASSIFIED	1058
5450	46881609 (8821, 8822)			UNCLASSIFIED	1037
5451	80412188 (8827, 8828)			UNCLASSIFIED	1024, 1029, 1038
5452	19881199 (8831, 8832)			UNCLASSIFIED	1034
5453	30790702 (8833, 8834)			UNCLASSIFIED	1003
5454	65902996 (8849, 8850)			UNCLASSIFIED	1023
5455	78380097 (8861, 8862)			UNCLASSIFIED	1008
5456	56073979 (8869, 8870)			UNCLASSIFIED	1021
5457	65658757 (8875, 8876)			UNCLASSIFIED	1054
5458	16340141 (8877, 8878)			UNCLASSIFIED	1022
5459	79327614 (8909, 8910)			UNCLASSIFIED	1009, 1053
5460	82482238 (8921, 8922)			UNCLASSIFIED	1001, 1008, 1025, 1044
5461	78967938 (8929, 8930)			UNCLASSIFIED	1037, 1038
5462	35107327 (8931, 8932)			UNCLASSIFIED	1030
5463	99102132 (8937, 8938)			UNCLASSIFIED	1006, 1010, 1012, 1023, 1024, 1025, 1054

5464	79852648 (8939, 8940)			UNCLASSIFIED	1017
5465	86463071 (8943, 8944)			UNCLASSIFIED	1007, 1048
5466	66149385 (8945, 8946)			UNCLASSIFIED	1004
5467	78798432 (8953, 8954)			UNCLASSIFIED	1009
5468	55285269 (8959, 8960)			UNCLASSIFIED	1029, 1053
5469	78386457 (8971, 8972)			UNCLASSIFIED	1003
5470	10173530 (8975, 8976)			UNCLASSIFIED	1039
5471	78160267 (8983, 8984)			UNCLASSIFIED	1024
5472	14160467 (8989, 8990)			UNCLASSIFIED	1053
5473	65888071 (8991, 8992)			UNCLASSIFIED	1054
5474	88078553 (9005, 9006)			UNCLASSIFIED	1008, 1036
5475	65988879 (9017, 9018)			UNCLASSIFIED	1016
5476	54846368 (9033, 9034)			UNCLASSIFIED	1041
5477	27981592 (9039, 9040)			UNCLASSIFIED	1006
5478	11698161 (9051, 9052)			UNCLASSIFIED	1031
5479	38895394 (9053, 9054)			UNCLASSIFIED	1037
5480	19888209 (9059, 9060)			UNCLASSIFIED	1001
5481	77948077 (9081, 9082)			UNCLASSIFIED	1019, 1021, 1041

5482	9873711 (9095, 9096)			UNCLASSIFIED	1017
5483	10328802 (9105, 9106)			UNCLASSIFIED	1025
5484	19876815 (9129, 9130)			UNCLASSIFIED	1034
5485	25263473 (9141, 9142)			UNCLASSIFIED	1022, 1027
5486	27989240 (9145, 9146)			UNCLASSIFIED	1016
5487	35908087 (9147, 9148)			UNCLASSIFIED	1029
5488	79407666 (9149, 9150)			UNCLASSIFIED	1016
5489	65659192 (9151, 9152)			UNCLASSIFIED	1016
5490	66051947 (9155, 9156)			UNCLASSIFIED	1009, 1049
5491	27999832 (9163, 9164)			UNCLASSIFIED	1039
5492	79410463 (9173, 9174)			UNCLASSIFIED	1022, 1024
5493	77528168 (9183, 9184)			UNCLASSIFIED	1038
5494	12952225 (9213, 9214)			UNCLASSIFIED	1024
5495	80079974 (9221, 9222)			UNCLASSIFIED	1034
5496	86681850 (9225, 9226)			UNCLASSIFIED	1007
5497	78381376 (9235, 9236)			UNCLASSIFIED	1007, 1026
5498	13084470 (9237, 9238)			UNCLASSIFIED	1031
5499	56516660 (9271, 9272)			UNCLASSIFIED	1009

5500	78743384 (9275, 9276)			UNCLASSIFIED	1022
5501	66998476 (9277, 9278)			UNCLASSIFIED	1038
5502	35106069 (9297, 9298)			UNCLASSIFIED	1026
5503	78793562 (9319, 9320)			UNCLASSIFIED	1026
5504	19740303 (9325, 9326)			UNCLASSIFIED	1003
5505	27348050 (9327, 9328)			UNCLASSIFIED	1026
5506	79558086 (9333, 9334)			UNCLASSIFIED	1025
5507	65468647 (9365, 9366)			UNCLASSIFIED	1054
5508	86684698 (9385, 9386)			UNCLASSIFIED	1029
5509	19524167 (9389, 9390)			UNCLASSIFIED	1024
5510	91220456 (9403, 9404)			UNCLASSIFIED	1016, 1044
5511	85808289 (9417, 9418)			UNCLASSIFIED	1038
5512	65886745 (9427, 9428)			UNCLASSIFIED	1016
5513	65706400 (9429, 9430)			UNCLASSIFIED	1038
5514	25146194 (9439, 9440)			UNCLASSIFIED	1026
5515	80504729 (9445, 9446)			UNCLASSIFIED	1012
5516	78043389 (9451, 9452)			UNCLASSIFIED	1019, 1024
5517	79844495 (9457, 9458)			UNCLASSIFIED	1017

5518	65891771 (9463, 9454)			UNCLASSIFIED	1054
5519	9686476 (9493, 9494)			UNCLASSIFIED	1044
5520	91214067 (9497, 9498)			UNCLASSIFIED	1004, 1038, 1054
5521	33182707 (9499, 9500)			UNCLASSIFIED	1026
5522	55774697 (9505, 9506)			UNCLASSIFIED	1042
5523	79570642 (9515, 9516)			UNCLASSIFIED	1017
5524	16401672 (9517, 9518)			UNCLASSIFIED	1003
5525	11802897 (9519, 9520)			UNCLASSIFIED	1038
5526	78674539 (9525, 9526)			UNCLASSIFIED	1017
5527	20465812 (9539, 9540)			UNCLASSIFIED	1010
5528	27845638 (9551, 9552)			UNCLASSIFIED	1004
5529	79862271 (9563, 9564)			UNCLASSIFIED	1003
5530	80219133 (9573, 9574)			UNCLASSIFIED	1004, 1006, 1010, 1022, 1023, 1024, 1029
5531	35065361 (9575, 9576)			UNCLASSIFIED	1054
5532	56155951 (9583, 9584)			UNCLASSIFIED	1021
5533	37035315 (9591, 9592)			UNCLASSIFIED	1012
5534	82053475 (9599, 9600)			UNCLASSIFIED	1016, 1025
5535	17113146 (9605, 9606)			UNCLASSIFIED	1030

5536	8757940 (9613, 9614)			UNCLASSIFIED	1004
5537	28483261 (9619, 9620)			UNCLASSIFIED	1017
5538	78297749 (9635, 9636)			UNCLASSIFIED	1026
5539	17112442 (9639, 9640)			UNCLASSIFIED	1017
5540	79796290 (9663, 9664)			UNCLASSIFIED	1006, 1044
5541	66393096 (9673, 9674)			UNCLASSIFIED	1038
5542	10193406 (9689, 9690)			UNCLASSIFIED	1003, 1034
5543	87112156 (9699, 9700)			UNCLASSIFIED	1018, 1029
5544	10887205 (9703, 9704)			UNCLASSIFIED	1027
5545	8488525 (9711, 9712)			UNCLASSIFIED	1022
5546	28390930 (9729, 9730)			UNCLASSIFIED	1044
5547	56069022 (9733, 9734)			UNCLASSIFIED	1021
5548	11696202 (9743, 9744)			UNCLASSIFIED	1034
5549	94234080 (9747, 9748)			UNCLASSIFIED	1054
5550	23295902 (9763, 9764)			UNCLASSIFIED	1008
5551	20754580 (9771, 9772)			UNCLASSIFIED	1053
5552	79814789 (9781, 9782)			UNCLASSIFIED	1017
5553	79564903 (9785, 9786)			UNCLASSIFIED	1001

5554	30516871 (9797, 9798)			UNCLASSIFIED	1054
5555	66173108 (9809, 9810)			UNCLASSIFIED	1016
5556	79846238 (9813, 9814)			UNCLASSIFIED	1034
5557	79635469 (9817, 9818)			UNCLASSIFIED	1008
5558	25258306 (9823, 9824)			UNCLASSIFIED	1026
5559	25143575 (9825, 9826)			UNCLASSIFIED	1008
5560	87844752 (9837, 9838)			UNCLASSIFIED	1022, 1026
5561	16790707 (9843, 9844)			UNCLASSIFIED	1044
5562	94146857 (9847, 9848)			UNCLASSIFIED	1003
5563	94148515 (9851, 9852)			UNCLASSIFIED	1003
5564	36618675 (9853, 9854)			UNCLASSIFIED	1053
5565	20283588 (9855, 9856)			UNCLASSIFIED	1022
5566	17956663 (9885, 9886)			UNCLASSIFIED	1023
5567	25316725 (9889, 9890)			UNCLASSIFIED	1008
5568	35055197 (9899, 9900)			UNCLASSIFIED	1054
5569	78362601 (9903, 9904)			UNCLASSIFIED	1003
5570	35137716 (9913, 9914)			UNCLASSIFIED	1050
5571	20286406 (9915, 9916)			UNCLASSIFIED	1022

5572	56513763 (9925, 9926)			UNCLASSIFIED	1019
5573	65506331 (9931, 9932)			UNCLASSIFIED	1016
5574	79829867 (9943, 9944)			UNCLASSIFIED	1003
5575	20084286 (9959, 9960)			UNCLASSIFIED	1034, 1038
5576	79816963 (9969, 9970)			UNCLASSIFIED	1003, 1039
5577	78784691 (9983, 9984)			UNCLASSIFIED	1008
5578	94986285 (9987, 9988)			UNCLASSIFIED	1006, 1022, 1024, 1039
5579	34118129 (10005, 10006)			UNCLASSIFIED	1000
5580	20750713 (10021, 10022)			UNCLASSIFIED	1022
5581	80232467 (10027, 10028)			UNCLASSIFIED	1022, 1023, 1034, 1044, 1053
5582	46777580 (10029, 10030)			UNCLASSIFIED	1021
5583	11122569 (10045, 10046)			UNCLASSIFIED	1053
5584	86687237 (10053, 10054)			UNCLASSIFIED	1007
5585	57301313 (10075, 10076)			UNCLASSIFIED	1004, 1008, 1022, 1024, 1034
5586	28462264 (10077, 10078)			UNCLASSIFIED	1003
5587	30749180 (10081, 10082)			UNCLASSIFIED	1053
5588	85516018 (10089, 10090)			UNCLASSIFIED	1049
5589	29346656 (10091, 10092)			UNCLASSIFIED	1022

5590	79610411 (10093, 10094)			UNCLASSIFIED	1039
5591	77806491 (10095, 10096)			UNCLASSIFIED	1054
5592	25258987 (10101, 10102)			UNCLASSIFIED	1008
5593	46781301 (10107, 10108)			UNCLASSIFIED	1036
5594	24134290 (10113, 10114)			UNCLASSIFIED	1009
5595	79966305 (10115, 10116)			UNCLASSIFIED	1003, 1008
5596	12995756 (10123, 10124)			UNCLASSIFIED	1031
5597	70760894 (10141, 10142)			UNCLASSIFIED	1034
5598	9844485 (10163, 10164)			UNCLASSIFIED	1039
5599	10199719 (10171, 10172)			UNCLASSIFIED	1004
5600	65860849 (10185, 10186)			UNCLASSIFIED	1006, 1044
5601	65694352 (10195, 10196)			UNCLASSIFIED	1023
5602	77707056 (10209, 10210)			UNCLASSIFIED	1044
5603	87467723 (10213, 10214)			UNCLASSIFIED	1018
5604	85816113 (10215, 10216)			UNCLASSIFIED	1019
5605	80502186 (10219, 10220)			UNCLASSIFIED	1012
5606	91228683 (10231, 10232)			UNCLASSIFIED	1010
5607	25260597 (10239, 10240)			UNCLASSIFIED	1008

5608	10279525 (10241, 10242)			UNCLASSIFIED	1038
5609	16300960 (10249, 10250)			UNCLASSIFIED	1054
5610	20630358 (10257, 10258)			UNCLASSIFIED	1004
5611	79391995 (10261, 10262)			UNCLASSIFIED	1006, 1058
5612	80421046 (10263, 10264)			UNCLASSIFIED	1017, 1025
5613	80255237 (10281, 10282)			UNCLASSIFIED	1004, 1039
5614	78386464 (10285, 10286)			UNCLASSIFIED	1008, 1026
5615	78930589 (10299, 10300)			UNCLASSIFIED	1054
5616	30539361 (10305, 10306)			UNCLASSIFIED	1026
5617	78906843 (10307, 10308)			UNCLASSIFIED	1023, 1037
5618	46854297 (10317, 10318)			UNCLASSIFIED	1029
5619	20262916 (10321, 10322)			UNCLASSIFIED	1034
5620	16427755 (10337, 10338)			UNCLASSIFIED	1016
5621	8213493 (10343, 10344)			UNCLASSIFIED	1022
5622	54995422 (10355, 10356)			UNCLASSIFIED	1029
5623	87111945 (10359, 10360)			UNCLASSIFIED	1007
5624	79825759 (10361, 10362)			UNCLASSIFIED	1044
5625	11398291 (10371, 10372)			UNCLASSIFIED	1006

5626	16311252 (10373, 10374)			UNCLASSIFIED	1054
5627	23289740 (10379, 10380)			UNCLASSIFIED	1039
5628	19726070 (10385, 10386)			UNCLASSIFIED	1001
5629	79769400 (10395, 10396)			UNCLASSIFIED	1023
5630	78393145 (10405, 10406)			UNCLASSIFIED	1038
5631	79187152 (10409, 10410)			UNCLASSIFIED	1024
5632	28480089 (10423, 10424)			UNCLASSIFIED	1008
5633	78307291 (10431, 10432)			UNCLASSIFIED	1010, 1021, 1026, 1042, 1050
5634	94134692 (10439, 10440)			UNCLASSIFIED	1010, 1016, 1023
5635	78296125 (10441, 10442)			UNCLASSIFIED	1026, 1038
5636	7423129 (10443, 10444)			UNCLASSIFIED	1058
5637	36999845 (10449, 10450)			UNCLASSIFIED	1001
5638	94852367 (10453, 10454)			UNCLASSIFIED	1044
5639	28991438 (10459, 10460)			UNCLASSIFIED	1022
5640	20465281 (10473, 10474)			UNCLASSIFIED	1010
5641	19881808 (10475, 10476)			UNCLASSIFIED	1034
5642	25316013 (10479, 10480)			UNCLASSIFIED	1008
5643	35104971 (10505, 10506)			UNCLASSIFIED	1029

5644	88095343 (10507, 10508)			UNCLASSIFIED	1003, 1004, 1006, 1008, 1010, 1012, 1017, 1022, 1026, 1034, 1044
5645	78955994 (10529, 10530)			UNCLASSIFIED	1008
5646	48891680 (10531, 10532)			UNCLASSIFIED	1019
5647	10090155 (10551, 10552)			UNCLASSIFIED	1017
5648	94147972 (10569, 10570)			UNCLASSIFIED	1044
5649	65668068 (10579, 10580)			UNCLASSIFIED	1063
5650	79471521 (10639, 10640)			UNCLASSIFIED	1038
5651	78794826 (10647, 10648)			UNCLASSIFIED	1023
5652	28775148 (10659, 10660)			UNCLASSIFIED	1017
5653	94134697 (10665, 10666)			UNCLASSIFIED	1003
5654	11243179 (10685, 10686)			UNCLASSIFIED	1010
5655	37004946 (10689, 10690)			UNCLASSIFIED	1029
5656	11122121 (10691, 10692)			UNCLASSIFIED	1022
5657	80226630 (10693, 10694)			UNCLASSIFIED	1022
5658	32149728 (10695, 10696)			UNCLASSIFIED	1029
5659	79441310 (10697, 10698)			UNCLASSIFIED	1001, 1016
5660	20432776 (10719, 10720)			UNCLASSIFIED	1024

5661	98951544 (10725, 10726)			UNCLASSIFIED	1025, 1038, 1042
5662	94132198 (10735, 10736)			UNCLASSIFIED	1003, 1022
5663	78706056 (10747, 10748)			UNCLASSIFIED	1025
5664	11707882 (10751, 10752)			UNCLASSIFIED	1031
5665	16338333 (10765, 10766)			UNCLASSIFIED	1010
5666	28463541 (10773, 10774)			UNCLASSIFIED	1024
5667	33207901 (10775, 10776)			UNCLASSIFIED	1026
5668	29891912 (10783, 10784)			UNCLASSIFIED	1024
5669	78459861 (10807, 10808)			UNCLASSIFIED	1026
5670	79617635 (10813, 10814)			UNCLASSIFIED	1003
5671	20608797 (10831, 10832)			UNCLASSIFIED	1004
5672	85528433 (10843, 10844)			UNCLASSIFIED	1016, 1038
5673	79966785 (10847, 10848)			UNCLASSIFIED	1003, 1038, 1054
5674	79489975 (10853, 10854)			UNCLASSIFIED	1038
5675	79116753 (10869, 10870)			UNCLASSIFIED	1013
5676	20287505 (10875, 10876)			UNCLASSIFIED	1034
5677	79314110 (10883, 10884)			UNCLASSIFIED	1022, 1058
5678	79607120 (10885, 10886)			UNCLASSIFIED	1001, 1036, 1050

5679	46676790 (10887, 10888)			UNCLASSIFIED	1054
5680	37062168 (10889, 10890)			UNCLASSIFIED	1054
5681	65893063 (10899, 10900)			UNCLASSIFIED	1054
5682	94239912 (10907, 10908)			UNCLASSIFIED	1039
5683	46853046 (10909, 10910)			UNCLASSIFIED	1037
5684	78489931 (10915, 10916)			UNCLASSIFIED	1054
5685	20466896 (10923, 10924)			UNCLASSIFIED	1010
5686	85814060 (10939, 10940)			UNCLASSIFIED	1038
5687	30631955 (10943, 10944)			UNCLASSIFIED	1022
5688	65884532 (10949, 10950)			UNCLASSIFIED	1054
5689	17882450 (10969, 10970)			UNCLASSIFIED	1039
5690	78707221 (10971, 10972)			UNCLASSIFIED	1039
5691	30526078 (10979, 10980)			UNCLASSIFIED	1012
5692	28479005 (10981, 10982)			UNCLASSIFIED	1022
5693	16750434 (10991, 10992)			UNCLASSIFIED	1039
5694	77881613 (11007, 11008)			UNCLASSIFIED	1019
5695	85528260 (11017, 11018)			UNCLASSIFIED	1049
5696	34664696 (11019, 11020)			UNCLASSIFIED	1024

5697	98811078 (11021, 11022)			UNCLASSIFIED	1008, 1010, 1058
5698	17885580 (11023, 11024)			UNCLASSIFIED	1024
5699	78077942 (11025, 11026)			UNCLASSIFIED	1029
5700	46775729 (11027, 11028)			UNCLASSIFIED	1021
5701	55778000 (11043, 11044)			UNCLASSIFIED	1021
5702	85531395 (11045, 11046)			UNCLASSIFIED	1038
5703	11392476 (11049, 11050)			UNCLASSIFIED	1024
5704	65660735 (11077, 11078)			UNCLASSIFIED	1053
5705	91238820 (11083, 11084)			UNCLASSIFIED	1010
5706	57158191 (11085, 11086)			UNCLASSIFIED	1034
5707	78979937 (11087, 11088)			UNCLASSIFIED	1024, 1038
5708	78954675 (11091, 11092)			UNCLASSIFIED	1039
5709	81516220 (11103, 11104)			UNCLASSIFIED	1024, 1034, 1039, 1044, 1054, 1058
5710	21629822 (11105, 11106)			UNCLASSIFIED	1029
5711	93834450 (11111, 11112)			UNCLASSIFIED	1017
5712	80229608 (11113, 11114)			UNCLASSIFIED	1006
5713	78239349 (11119, 11120)			UNCLASSIFIED	1008, 1026
5714	78939376 (11131, 11132)			UNCLASSIFIED	1023

5715	94713900 (11133, 11134)			UNCLASSIFIED	1010
5716	82356540 (11135, 11136)			UNCLASSIFIED	1001, 1006, 1009, 1010, 1016, 1022, 1023, 1025, 1026, 1027, 1034, 1039, 1044, 1054
5717	81929227 (11137, 11138)			UNCLASSIFIED	1012, 1016, 1022, 1044
5718	66151358 (11149, 11150)			UNCLASSIFIED	1024
5719	79834402 (11161, 11162)			UNCLASSIFIED	1008
5720	10370165 (11185, 11186)			UNCLASSIFIED	1044
5721	11698624 (11215, 11216)			UNCLASSIFIED	1031
5722	29689480 (11225, 11226)			UNCLASSIFIED	1054
5723	78375454 (11239, 11240)			UNCLASSIFIED	1016, 1044, 1056
5724	46782308 (11243, 11244)			UNCLASSIFIED	1036
5725	5601181 (11245, 11246)			UNCLASSIFIED	1058
5726	49511773 (11257, 11258)			UNCLASSIFIED	1036
5727	16711666 (11261, 11262)			UNCLASSIFIED	1044
5728	43989154 (11271, 11272)			UNCLASSIFIED	1022
5729	17523511 (11275, 11276)			UNCLASSIFIED	1003
5730	79843241 (11279, 11280)			UNCLASSIFIED	1044

5731	98280054 (11287, 11288)			UNCLASSIFIED	1026, 1054
5732	11284944 (11297, 11298)			UNCLASSIFIED	1022
5733	78674631 (11301, 11302)			UNCLASSIFIED	1022
5734	78975613 (11303, 11304)			UNCLASSIFIED	1023
5735	20475173 (11313, 11314)			UNCLASSIFIED	1034
5736	11814786 (11315, 11316)			UNCLASSIFIED	1024
5737	17933825 (11331, 11332)			UNCLASSIFIED	1038
5738	78389805 (11337, 11338)			UNCLASSIFIED	1008
5739	10047151 (11341, 11342)			UNCLASSIFIED	1003
5740	16460451 (11373, 11374)			UNCLASSIFIED	1023
5741	52561245 (11375, 11376)			UNCLASSIFIED	1017
5742	27972629 (11381, 11382)			UNCLASSIFIED	1053
5743	88166396 (11383, 11384)			UNCLASSIFIED	1006, 1008, 1023, 1024, 1026, 1034, 1039
5744	99385600 (11393, 11394)			UNCLASSIFIED	1017, 1039
5745	79582720 (11395, 11396)			UNCLASSIFIED	1027
5746	65900847 (11397, 11398)			UNCLASSIFIED	1012, 1023
5747	11293031 (11415, 11416)			UNCLASSIFIED	1010
5748	35913706 (11419, 11420)			UNCLASSIFIED	1029

5749	11380635 (11451, 11452)			UNCLASSIFIED	1016
5750	39517795 (11455, 11456)			UNCLASSIFIED	1006
5751	9874851 (11457, 11458)			UNCLASSIFIED	1044
5752	78728822 (11459, 11460)			UNCLASSIFIED	1022
5753	80080839 (11461, 11462)			UNCLASSIFIED	1001, 1034
5754	66395865 (11467, 11468)			UNCLASSIFIED	1009
5755	79558181 (11469, 11470)			UNCLASSIFIED	1038
5756	65898006 (11475, 11476)			UNCLASSIFIED	1054
5757	79621395 (11477, 11478)			UNCLASSIFIED	1003
5758	20292105 (11495, 11496)			UNCLASSIFIED	1034
5759	39466729 (11515, 11516)			UNCLASSIFIED	1004
5760	46863141 (11517, 11518)			UNCLASSIFIED	1050
5761	86379982 (11521, 11522)			UNCLASSIFIED	1053
5762	79632973 (11529, 11530)			UNCLASSIFIED	1038
5763	55299529 (11533, 11534)			UNCLASSIFIED	1029
5764	11090092 (11571, 11572)			UNCLASSIFIED	1006
5765	96200178 (11577, 11578)			UNCLASSIFIED	1025
5766	27967667 (11603, 11604)			UNCLASSIFIED	1053

5767	80224053 (11611, 11612)			UNCLASSIFIED	1022, 1027
5768	27362132 (11619, 11620)			UNCLASSIFIED	1026
5769	79222407 (11631, 11632)			UNCLASSIFIED	1003, 1008, 1010, 1026
5770	79777614 (11637, 11638)			UNCLASSIFIED	1008, 1017
5771	65484453 (11659, 11660)			UNCLASSIFIED	1038
5772	19893798 (11663, 11664)			UNCLASSIFIED	1034
5773	21414303 (11665, 11666)			UNCLASSIFIED	1024
5774	35905367 (11669, 11670)			UNCLASSIFIED	1029
5775	46871053 (11673, 11674)			UNCLASSIFIED	1022
5776	25254883 (11681, 11682)			UNCLASSIFIED	1026
5777	9668350 (11699, 11700)			UNCLASSIFIED	1034
5778	94134826 (11701, 11702)			UNCLASSIFIED	1010, 1038
5779	79209852 (11713, 11714)			UNCLASSIFIED	1054
5780	79810843 (11729, 11730)			UNCLASSIFIED	1017, 1054
5781	20432511 (11769, 11770)			UNCLASSIFIED	1022
5782	78182358 (11775, 11776)			UNCLASSIFIED	1026, 1029, 1040, 1053
5783	9679326 (11781, 11782)			UNCLASSIFIED	1044
5784	78962171 (11783, 11784)			UNCLASSIFIED	1039

5785	87466217 (11785, 11786)			UNCLASSIFIED	1018
5786	79252239 (11787, 11788)			UNCLASSIFIED	1008, 1016, 1024, 1038
5787	56714299 (11799, 11800)			UNCLASSIFIED	1016, 1036
5788	91235092 (11803, 11804)			UNCLASSIFIED	1010
5789	55005621 (11815, 11816)			UNCLASSIFIED	1019
5790	80420019 (11835, 11836)			UNCLASSIFIED	1001, 1008, 1017, 1025, 1038, 1044
5791	95199434 (11851, 11852)			UNCLASSIFIED	1029
5792	13518686 (11871, 11872)			UNCLASSIFIED	1034
5793	94652279 (11879, 11880)			UNCLASSIFIED	1006
5794	55929780 (11883, 11884)			UNCLASSIFIED	1010
5795	78444786 (11885, 11886)			UNCLASSIFIED	1026
5796	80200986 (11893, 11894)			UNCLASSIFIED	1022, 1023, 1024
5797	79559331 (11899, 11900)			UNCLASSIFIED	1039
5798	8757228 (11917, 11918)			UNCLASSIFIED	1004
5799	79441478 (11927, 11928)			UNCLASSIFIED	1022
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5801	80248700 (11949, 11950)			UNCLASSIFIED	1006, 1008
5802	65981457 (11957, 11958)			UNCLASSIFIED	1024, 1027

5803	12916245 (11971, 11972)			UNCLASSIFIED	1024
5804	77797341 (11987, 11988)			UNCLASSIFIED	1051
5805	79810441 (11989, 11990)			UNCLASSIFIED	1004, 1008, 1017
5806	10300902 (11993, 11994)			UNCLASSIFIED	1001
5807	11685240 (12001, 12002)			UNCLASSIFIED	1016
5808	20748452 (12009, 12010)			UNCLASSIFIED	1022
5809	78187997 (12011, 12012)			UNCLASSIFIED	1029
5810	79582969 (12021, 12022)			UNCLASSIFIED	1022
5811	80055035 (12029, 12030)			UNCLASSIFIED	1004, 1010, 1012, 1027, 1034
5812	46571939 (12033, 12034)			UNCLASSIFIED	1029, 1053
5813	71731235 (12043, 12044)			UNCLASSIFIED	1003
5814	29143572 (12045, 12046)			UNCLASSIFIED	1017
5815	30247621 (12049, 12050)			UNCLASSIFIED	1030
5816	55005916 (12055, 12056)			UNCLASSIFIED	1019
5817	29345971 (12077, 12078)			UNCLASSIFIED	1022
5818	80549299 (12101, 12102)			UNCLASSIFIED	1016, 1023, 1024, 1058
5819	32287381 (12109, 12110)			UNCLASSIFIED	1029
5820	86473933 (12131, 12132)			UNCLASSIFIED	1054

5821	94144140 (12133, 12134)			UNCLASSIFIED	1003
5822	65668721 (12135, 12136)			UNCLASSIFIED	1016
5823	11809291 (12145, 12146)			UNCLASSIFIED	1038
5824	20435968 (12155, 12156)			UNCLASSIFIED	1024
5825	13086282 (12169, 12170)			UNCLASSIFIED	1024
5826	79973785 (12189, 12190)			UNCLASSIFIED	1023
5827	21422499 (12197, 12198)			UNCLASSIFIED	1004
5828	19514022 (12207, 12208)			UNCLASSIFIED	1022
5829	20632844 (12213, 12214)			UNCLASSIFIED	1004
5830	78461254 (12239, 12240)			UNCLASSIFIED	1008, 1026
5831	34129023 (12263, 12264)			UNCLASSIFIED	1026
5832	47656539 (12267, 12268)			UNCLASSIFIED	1029
5833	78254650 (12269, 12270)			UNCLASSIFIED	1026
5834	27978283 (12271, 12272)			UNCLASSIFIED	1022
5835	20727944 (12281, 12282)			UNCLASSIFIED	1006
5836	99413052 (12285, 12286)			UNCLASSIFIED	1001, 1008, 1010, 1017, 1023, 1037, 1044, 1054
5837	35906642 (12329, 12330)			UNCLASSIFIED	1029

5838	79633207 (12363, 12364)			UNCLASSIFIED	1039
5839	79828750 (12365, 12366)			UNCLASSIFIED	1039
5840	81774665 (12367, 12368)			UNCLASSIFIED	1008, 1016, 1023, 1025, 1029, 1034, 1054, 1058
5841	30538258 (12369, 12370)			UNCLASSIFIED	1016
5842	79211640 (12371, 12372)			UNCLASSIFIED	1054
5843	79866572 (12387, 12388)			UNCLASSIFIED	1038
5844	23297387 (12409, 12410)			UNCLASSIFIED	1008
5845	80089874 (12413, 12414)			UNCLASSIFIED	1010, 1016, 1054
5846	79159603 (12427, 12428)			UNCLASSIFIED	1004, 1009, 1022, 1026, 1039, 1053
5847	24133255 (12443, 12444)			UNCLASSIFIED	1003
5848	11758131 (12459, 12460)			UNCLASSIFIED	1025
5849	80079014 (12475, 12476)			UNCLASSIFIED	1034
5850	78381206 (12495, 12496)			UNCLASSIFIED	1039
5851	94133459 (12503, 12504)			UNCLASSIFIED	1022, 1045
5852	66313988 (12521, 12522)			UNCLASSIFIED	1016, 1054
5853	79420151 (12523, 12524)			UNCLASSIFIED	1024
5854	28348581 (12529, 12530)			UNCLASSIFIED	1024

5873	29367185 (12731, 12732)			UNCLASSIFIED	1026
5874	20622170 (12759, 12760)			UNCLASSIFIED	1004
5875	19539786 (12775, 12776)			UNCLASSIFIED	1003
5876	65475251 (12787, 12788)			UNCLASSIFIED	1038
5877	65469684 (12801, 12802)			UNCLASSIFIED	1038
5878	78408108 (12821, 12822)			UNCLASSIFIED	1024
5879	11760547 (12829, 12830)			UNCLASSIFIED	1038
5880	32311406 (12853, 12854)			UNCLASSIFIED	1029
5881	78767260 (12863, 12864)			UNCLASSIFIED	1030
5882	87463992 (12869, 12870)			UNCLASSIFIED	1018
5883	9874073 (12873, 12874)			UNCLASSIFIED	1044
5884	78955204 (12877, 12878)			UNCLASSIFIED	1017
5885	8499175 (12879, 12880)			UNCLASSIFIED	1022
5886	13076808 (12891, 12892)			UNCLASSIFIED	1022
5887	85541794 (12899, 12900)			UNCLASSIFIED	1054
5888	23015543 (12903, 12904)			UNCLASSIFIED	1039
5889	46668410 (12905, 12906)			UNCLASSIFIED	1022
5890	86679917 (12911, 12912)			UNCLASSIFIED	1007

5891	94312044 (12931, 12932)			UNCLASSIFIED	1023, 1035
5892	17937413 (12933, 12934)			UNCLASSIFIED	1039
5893	30646264 (12935, 12936)			UNCLASSIFIED	1008
5894	79241532 (12945, 12946)			UNCLASSIFIED	1003, 1016, 1017, 1023, 1024, 1038, 1039, 1044
5895	21149067 (12951, 12952)			UNCLASSIFIED	1058
5896	65874895 (12957, 12958)			UNCLASSIFIED	1054
5897	5823647 (12963, 12964)			UNCLASSIFIED	1058
5898	79836111 (12981, 12982)			UNCLASSIFIED	1044
5899	20459851 (12983, 12984)			UNCLASSIFIED	1024
5900	79842912 (12985, 12986)			UNCLASSIFIED	1004, 1008, 1044
5901	94121682 (13031, 13032)			UNCLASSIFIED	1054
5902	79777270 (13043, 13044)			UNCLASSIFIED	1017
5903	33765065 (13045, 13046)			UNCLASSIFIED	1026
5904	94555391 (13049, 13050)			UNCLASSIFIED	1001, 1006, 1008, 1010, 1024, 1034, 1039, 1058
5905	35100519 (13067, 13068)			UNCLASSIFIED	1024
5906	24120097 (13071, 13072)			UNCLASSIFIED	1026

5907	10370184 (13075, 13076)			UNCLASSIFIED	1044
5908	87128876 (13093, 13094)			UNCLASSIFIED	1007, 1013, 1016, 1025, 1029, 1034, 1044, 1048
5909	7797987 (13113, 13114)			UNCLASSIFIED	1054
5910	65490646 (13137, 13138)			UNCLASSIFIED	1023
5911	65468664 (13141, 13142)			UNCLASSIFIED	1054
5912	37013642 (13151, 13152)			UNCLASSIFIED	1029
5913	78978053 (13163, 13164)			UNCLASSIFIED	1054
5914	25327049 (13175, 13176)			UNCLASSIFIED	1003
5915	78708986 (13177, 13178)			UNCLASSIFIED	1003
5916	80060983 (13179, 13180)			UNCLASSIFIED	1024, 1039
5917	16549443 (13187, 13188)			UNCLASSIFIED	1003
5918	79914604 (13225, 13226)			UNCLASSIFIED	1006, 1024, 1025
5919	20728402 (13235, 13236)			UNCLASSIFIED	1006
5920	66396359 (13251, 13252)			UNCLASSIFIED	1008
5921	35933698 (13253, 13254)			UNCLASSIFIED	1053
5922	78513264 (13257, 13258)			UNCLASSIFIED	1030
5923	78087821 (13273, 13274)			UNCLASSIFIED	1050

5924	57306249 (13283, 13284)			UNCLASSIFIED	1003, 1004, 1006, 1009, 1010, 1022, 1023, 1024, 1034, 1039
5925	79865642 (13285, 13286)			UNCLASSIFIED	1017
5926	65896592 (13289, 13290)			UNCLASSIFIED	1038, 1054
5927	36746287 (13293, 13294)			UNCLASSIFIED	1034
5928	19641216 (13305, 13306)			UNCLASSIFIED	1022
5929	79238311 (13313, 13314)			UNCLASSIFIED	1008
5930	32305008 (13335, 13336)			UNCLASSIFIED	1001
5931	79876183 (13339, 13340)			UNCLASSIFIED	1017
5932	36624062 (13345, 13346)			UNCLASSIFIED	1034
5933	65897823 (13347, 13348)			UNCLASSIFIED	1054
5934	79810858 (13359, 13360)			UNCLASSIFIED	1017
5935	33200150 (13365, 13366)			UNCLASSIFIED	1050
5936	30254615 (13369, 13370)			UNCLASSIFIED	1026
5937	32679569 (13371, 13372)			UNCLASSIFIED	1012
5938	79265479 (13377, 13378)			UNCLASSIFIED	1013
5939	11769693 (13387, 13388)			UNCLASSIFIED	1038
5940	51219685 (13395, 13396)			UNCLASSIFIED	1036

5941	77659114 (13399, 13400)			UNCLASSIFIED	1054
5942	24129461 (13407, 13408)			UNCLASSIFIED	1003
5943	56329354 (13429, 13430)			UNCLASSIFIED	1030
5944	10278706 (13435, 13436)			UNCLASSIFIED	1025
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5946	80062425 (13441, 13442)			UNCLASSIFIED	1010
5947	66694286 (13447, 13448)			UNCLASSIFIED	1009
5948	66397495 (13463, 13464)			UNCLASSIFIED	1008, 1030
5949	80027645 (13475, 13476)			UNCLASSIFIED	1006
5950	55769575 (13489, 13490)			UNCLASSIFIED	1038
5951	77474508 (13491, 13492)			UNCLASSIFIED	1023
5952	94255974 (13499, 13500)			UNCLASSIFIED	1008
5953	82205191 (13509, 13510)			UNCLASSIFIED	1004, 1006, 1009, 1016, 1022, 1034
5954	78680880 (13537, 13538)			UNCLASSIFIED	1009, 1022
5955	81793888 (13547, 13548)			UNCLASSIFIED	1010, 1023, 1038, 1044, 1054
5956	54994478 (13551, 13552)			UNCLASSIFIED	1029
5957	86476573 (13559, 13560)			UNCLASSIFIED	1029
5958	79627829 (13575, 13576)			UNCLASSIFIED	1039

5959	6329693 (13585, 13586)			UNCLASSIFIED	1058
5960	80079026 (13591, 13592)			UNCLASSIFIED	1034
5961	86477481 (13593, 13594)			UNCLASSIFIED	1029
5962	79640376 (13599, 13600)			UNCLASSIFIED	1025
5963	87899013 (13605, 13606)			UNCLASSIFIED	1015
5964	71837603 (13619, 13620)			UNCLASSIFIED	1016, 1030
5965	32339114 (13633, 13634)			UNCLASSIFIED	1029
5966	20262354 (13635, 13636)			UNCLASSIFIED	1034
5967	65902508 (13643, 13644)			UNCLASSIFIED	1010
5968	88096986 (13651, 13652)			UNCLASSIFIED	1025
5969	20286074 (13663, 13664)			UNCLASSIFIED	1022
5970	20484824 (13679, 13680)			UNCLASSIFIED	1022
5971	80056066 (13681, 13682)			UNCLASSIFIED	1022
5972	50104079 (13689, 13690)			UNCLASSIFIED	1036
5973	52211502 (13697, 13698)			UNCLASSIFIED	1036
5974	11814410 (13701, 13702)			UNCLASSIFIED	1006
5975	19517954 (13719, 13720)			UNCLASSIFIED	1003
5976	52382453 (13731, 13732)			UNCLASSIFIED	1036

5977	91237050 (13735, 13736)			UNCLASSIFIED	1010
5978	30169544 (13743, 13744)			UNCLASSIFIED	1030
5979	38439143 (13745, 13746)			UNCLASSIFIED	1054
5980	28787444 (13747, 13748)			UNCLASSIFIED	1017, 1039
5981	95103762 (13765, 13766)			UNCLASSIFIED	1003
5982	27966169 (13769, 13770)			UNCLASSIFIED	1006
5983	79816745 (13777, 13778)			UNCLASSIFIED	1003
5984	78375927 (13779, 13780)			UNCLASSIFIED	1004, 1008, 1026
5985	24135857 (13789, 13790)			UNCLASSIFIED	1003
5986	25336368 (13793, 13794)			UNCLASSIFIED	1003
5987	38865169 (13795, 13796)			UNCLASSIFIED	1044
5988	35129892 (13801, 13802)			UNCLASSIFIED	1012
5989	80155853 (13807, 13808)			UNCLASSIFIED	1042, 1058
5990	49613350 (13811, 13812)			UNCLASSIFIED	1036
5991	25341208 (13815, 13816)			UNCLASSIFIED	1003
5992	65861983 (13845, 13846)			UNCLASSIFIED	1038
5993	13518036 (13849, 13850)			UNCLASSIFIED	1024
5994	9277094 (13863, 13864)			UNCLASSIFIED	1004

5995	27957397 (13869, 13870)			UNCLASSIFIED	1022
5996	80499320 (13871, 13872)			UNCLASSIFIED	1012, 1027
5997	16295194 (13875, 13876)			UNCLASSIFIED	1054
5998	11813881 (13877, 13878)			UNCLASSIFIED	1006
5999	55307132 (13905, 13906)			UNCLASSIFIED	1019
6000	79779635 (13907, 13908)			UNCLASSIFIED	1003, 1008
6001	91213830 (13917, 13918)			UNCLASSIFIED	1024
6002	10248646 (13927, 13928)			UNCLASSIFIED	1038
6003	37009841 (13941, 13942)			UNCLASSIFIED	1029
6004	49103404 (13951, 13952)			UNCLASSIFIED	1040
6005	78676716 (13981, 13982)			UNCLASSIFIED	1009
6006	79201215 (13987, 13988)			UNCLASSIFIED	1054
6007	80073366 (13999, 14000)			UNCLASSIFIED	1012, 1024, 1031
6008	20466557 (14011, 14012)			UNCLASSIFIED	1010
6009	57294429 (14013, 14014)			UNCLASSIFIED	1003, 1004, 1016, 1022, 1023, 1024, 1026, 1034, 1038
6010	20718836 (14023, 14024)			UNCLASSIFIED	1053
6011	52232443 (14025, 14026)			UNCLASSIFIED	1036

6012	78920547 (14027, 14028)			UNCLASSIFIED	1039
6013	77813198 (14035, 14036)			UNCLASSIFIED	1054
6014	56301392 (14049, 14050)			UNCLASSIFIED	1024
6015	19752312 (14055, 14056)			UNCLASSIFIED	1016
6016	20706304 (14091, 14092)			UNCLASSIFIED	1024
6017	85516704 (14093, 14094)			UNCLASSIFIED	1003, 1004, 1017, 1023, 1053
6018	78315829 (14097, 14098)			UNCLASSIFIED	1026
6019	78765320 (14099, 14100)			UNCLASSIFIED	1008, 1044
6020	20736168 (14109, 14110)			UNCLASSIFIED	1034
6021	65671409 (14113, 14114)			UNCLASSIFIED	1016
6022	66408222 (14121, 14122)			UNCLASSIFIED	1034
6023	94684857 (14123, 14124)			UNCLASSIFIED	1027
6024	86675501 (14125, 14126)			UNCLASSIFIED	1007
6025	35906837 (14127, 14128)			UNCLASSIFIED	1026
6026	13522469 (14147, 14148)			UNCLASSIFIED	1006
6027	34129275 (14155, 14156)			UNCLASSIFIED	1026
6028	19543561 (14169, 14170)			UNCLASSIFIED	1017
6029	81815041 (14175, 14176)			UNCLASSIFIED	1009, 1012, 1016, 1024, 1038, 1054

6030	19635848 (14183, 14184)			UNCLASSIFIED	1006
6031	80059447 (14189, 14190)			UNCLASSIFIED	1024, 1034
6032	16414278 (14199, 14200)			UNCLASSIFIED	1038
6033	65467837 (14207, 14208)			UNCLASSIFIED	1054
6034	80250186 (14211, 14212)			UNCLASSIFIED	1022
6035	49602900 (14227, 14228)			UNCLASSIFIED	1036
6036	79590636 (14231, 14232)			UNCLASSIFIED	1003
6037	82062092 (14239, 14240)			UNCLASSIFIED	1012, 1016, 1022, 1023, 1031, 1049
6038	12986531 (14243, 14244)			UNCLASSIFIED	1004, 1023
6039	46866687 (14251, 14252)			UNCLASSIFIED	1037
6040	10264847 (14253, 14254)			UNCLASSIFIED	1038
6041	29227645 (14271, 14272)			UNCLASSIFIED	1030
6042	47652463 (14299, 14300)			UNCLASSIFIED	1029
6043	13033747 (14301, 14302)			UNCLASSIFIED	1027
6044	80254247 (14313, 14314)			UNCLASSIFIED	1001, 1004, 1006, 1008, 1010, 1017, 1024, 1038
6045	23286010 (14317, 14318)			UNCLASSIFIED	1003
6046	71770118 (14329, 14330)			UNCLASSIFIED	1008, 1035

6047	68990162 (14353, 14354)			UNCLASSIFIED	1009
6048	19900534 (14373, 14374)			UNCLASSIFIED	1054
6049	80025241 (14379, 14380)			UNCLASSIFIED	1004, 1008, 1025, 1026, 1027, 1031, 1034, 1039, 1044
6050	32445289 (14385, 14386)			UNCLASSIFIED	1029
6051	10359744 (14397, 14398)			UNCLASSIFIED	1039
6052	80251415 (14411, 14412)			UNCLASSIFIED	1010
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6054	77582797 (14429, 14430)			UNCLASSIFIED	1008
6055	34406413 (14441, 14442)			UNCLASSIFIED	1030
6056	78510094 (14453, 14454)			UNCLASSIFIED	1029
6057	78748347 (14459, 14460)			UNCLASSIFIED	1026
6058	11818389 (14487, 14488)			UNCLASSIFIED	1006
6059	49511790 (14505, 14506)			UNCLASSIFIED	1036
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6061	10370566 (14511, 14512)			UNCLASSIFIED	1017
6062	20227865 (14523, 14524)			UNCLASSIFIED	1022
6063	86457849 (14537, 14538)			UNCLASSIFIED	1019

6064	86469895 (14551, 14552)			UNCLASSIFIED	1029
6065	9863062 (14569, 14570)			UNCLASSIFIED	1008
6066	79834203 (14573, 14574)			UNCLASSIFIED	1008
6067	80408523 (14575, 14576)			UNCLASSIFIED	1006, 1029
6068	65451147 (14583, 14584)			UNCLASSIFIED	1016
6069	8500737 (14589, 14590)			UNCLASSIFIED	1024
6070	38912306 (14605, 14606)			UNCLASSIFIED	1008
6071	30230437 (14611, 14612)			UNCLASSIFIED	1026
6072	46885659 (14627, 14628)			UNCLASSIFIED	1034
6073	33184195 (14631, 14632)			UNCLASSIFIED	1026
6074	66432083 (14643, 14644)			UNCLASSIFIED	1024
6075	11763476 (14645, 14646)			UNCLASSIFIED	1038
6076	80089891 (14649, 14650)			UNCLASSIFIED	1024
6077	55663447 (14653, 14654)			UNCLASSIFIED	1021
6078	19726370 (14659, 14660)			UNCLASSIFIED	1038
6079	32728850 (14677, 14678)			UNCLASSIFIED	1001
6080	55402487 (14709, 14710)			UNCLASSIFIED	1019
6081	35910050 (14711, 14712)			UNCLASSIFIED	1029

6082	79642463 (14723, 14724)			UNCLASSIFIED	1003
6083	65892580 (14727, 14728)			UNCLASSIFIED	1016
6084	79556093 (14731, 14732)			UNCLASSIFIED	1003
6085	33763101 (14735, 14736)			UNCLASSIFIED	1026
6086	79822991 (14751, 14752)			UNCLASSIFIED	1039
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6088	39524195 (14771, 14772)			UNCLASSIFIED	1024
6089	95088346 (14777, 14778)			UNCLASSIFIED	1010, 1012
6090	39564789 (14807, 14808)			UNCLASSIFIED	1022
6091	78394792 (14809, 14810)			UNCLASSIFIED	1030
6092	82436757 (14819, 14820)			UNCLASSIFIED	1001
6093	79857010 (14827, 14828)			UNCLASSIFIED	1017
6094	79912418 (14833, 14834)			UNCLASSIFIED	1003, 1024, 1039
6095	20610299 (14847, 14848)			UNCLASSIFIED	1004, 1006, 1010, 1022, 1034
6096	7520373 (14851, 14852)			UNCLASSIFIED	1058
6097	94315759 (14861, 14862)			UNCLASSIFIED	1044
6098	66042360 (14869, 14870)			UNCLASSIFIED	1016, 1054
6099	28001705 (14889, 14890)			UNCLASSIFIED	1054

6100	79817946 (14897, 14898)			UNCLASSIFIED	1017
6101	71751873 (14899, 14900)			UNCLASSIFIED	1017
6102	46695963 (14911, 14912)			UNCLASSIFIED	1055
6103	29679831 (14913, 14914)			UNCLASSIFIED	1026
6104	78439125 (14921, 14922)			UNCLASSIFIED	1054
6105	10883732 (14925, 14926)			UNCLASSIFIED	1024
6106	79814879 (14929, 14930)			UNCLASSIFIED	1017
6107	20182170 (14939, 14940)			UNCLASSIFIED	1010
6108	80481798 (14941, 14942)			UNCLASSIFIED	1012, 1034
6109	78774280 (14943, 14944)			UNCLASSIFIED	1030, 1035
6110	79445447 (14949, 14950)			UNCLASSIFIED	1024
6111	87464570 (14953, 14954)			UNCLASSIFIED	1048
6112	91014513 (14973, 14974)			UNCLASSIFIED	1010
6113	20724615 (14983, 14984)			UNCLASSIFIED	1022
6114	20288874 (14985, 14986)			UNCLASSIFIED	1034
6115	79470492 (14991, 14992)			UNCLASSIFIED	1022
6116	79832064 (15013, 15014)			UNCLASSIFIED	1023
6117	10840979 (15015, 15016)			UNCLASSIFIED	1017

6118	9528784 (15025, 15026)			UNCLASSIFIED	1017
6119	10367865 (15047, 15048)			UNCLASSIFIED	1008
6120	20290685 (15053, 15054)			UNCLASSIFIED	1034
6121	65471547 (15067, 15068)			UNCLASSIFIED	1054
6122	78245105 (15073, 15074)			UNCLASSIFIED	1050
6123	80499691 (15075, 15076)			UNCLASSIFIED	1012
6124	30169721 (15085, 15086)			UNCLASSIFIED	1030
6125	27969515 (15091, 15092)			UNCLASSIFIED	1053
6126	80435976 (15101, 15102)			UNCLASSIFIED	1024, 1034, 1038, 1039, 1053, 1058
6127	32298653 (15113, 15114)			UNCLASSIFIED	1000
6128	65474183 (15119, 15120)			UNCLASSIFIED	1038
6129	20715643 (15121, 15122)			UNCLASSIFIED	1022
6130	65505758 (15133, 15134)			UNCLASSIFIED	1016, 1036
6131	17884741 (15135, 15136)			UNCLASSIFIED	1024
6132	79445908 (15137, 15138)			UNCLASSIFIED	1010
6133	65468678 (15139, 15140)			UNCLASSIFIED	1042, 1054
6134	95292733 (15157, 15158)			UNCLASSIFIED	1004, 1022
6135	81606240 (15169, 15170)			UNCLASSIFIED	1003, 1025, 1034, 1054

6136	52482921 (15181, 15182)			UNCLASSIFIED	1036
6137	80249237 (15185, 15186)			UNCLASSIFIED	1006, 1023
6138	85528846 (15187, 15188)			UNCLASSIFIED	1038
6139	11356609 (15193, 15194)			UNCLASSIFIED	1058
6140	8900447 (15201, 15202)			UNCLASSIFIED	1004
6141	6657173 (15207, 15208)			UNCLASSIFIED	1003, 1006, 1009, 1029
6142	17905313 (15217, 15218)			UNCLASSIFIED	1024
6143	39711115 (15265, 15266)			UNCLASSIFIED	1030
6144	80420041 (15267, 15268)			UNCLASSIFIED	1003, 1025
6145	49954326 (15279, 15280)			UNCLASSIFIED	1036
6146	27841955 (15285, 15286)			UNCLASSIFIED	1022
6147	17941363 (15303, 15304)			UNCLASSIFIED	1008
6148	29360575 (15307, 15308)			UNCLASSIFIED	1009
6149	11694135 (15323, 15324)			UNCLASSIFIED	1016
6150	20437235 (15353, 15354)			UNCLASSIFIED	1022
6151	17962664 (15375, 15376)			UNCLASSIFIED	1003
6152	37036201 (15381, 15382)			UNCLASSIFIED	1012
6153	21148407 (15393, 15394)			UNCLASSIFIED	1058

6154	78386135 (15421, 15422)			UNCLASSIFIED	1028
6155	79233705 (15425, 15426)			UNCLASSIFIED	1058
6156	68878005 (15441, 15442)			UNCLASSIFIED	1026, 1038
6157	47662156 (15447, 15448)			UNCLASSIFIED	1037
6158	13000633 (15449, 15450)			UNCLASSIFIED	1031
6159	71214081 (15453, 15454)			UNCLASSIFIED	1008, 1016, 1024, 1054
6160	46776147 (15469, 15470)			UNCLASSIFIED	1021
6161	29522216 (15475, 15476)			UNCLASSIFIED	1024
6162	94321055 (15515, 15516)			UNCLASSIFIED	1003, 1040
6163	29465102 (15523, 15524)			UNCLASSIFIED	1022
6164	38315439 (15525, 15526)			UNCLASSIFIED	1022
6165	10332787 (15529, 15530)			UNCLASSIFIED	1025
6166	70970283 (15537, 15538)			UNCLASSIFIED	1037
6167	79252908 (15539, 15540)			UNCLASSIFIED	1016
6168	80235376 (15545, 15546)			UNCLASSIFIED	1006, 1022
6169	78971479 (15569, 15570)			UNCLASSIFIED	1039
6170	78971675 (15575, 15576)			UNCLASSIFIED	1017
6171	46777800 (15579, 15580)			UNCLASSIFIED	1021

6172	55778366 (15585, 15586)			UNCLASSIFIED	1021
6173	20617381 (15591, 15592)			UNCLASSIFIED	1004
6174	79859183 (15601, 15602)			UNCLASSIFIED	1017, 1044, 1049
6175	34382799 (15635, 15636)			UNCLASSIFIED	1000
6176	79107926 (15645, 15646)			UNCLASSIFIED	1023
6177	20288041 (15649, 15650)			UNCLASSIFIED	1034
6178	78978200 (15655, 15656)			UNCLASSIFIED	1054
6179	28375850 (15683, 15684)			UNCLASSIFIED	1044
6180	80076624 (15691, 15692)			UNCLASSIFIED	1003, 1008, 1029, 1034, 1038
6181	20272040 (15697, 15698)			UNCLASSIFIED	1004
6182	30407363 (15723, 15724)			UNCLASSIFIED	1026
6183	65703781 (15725, 15726)			UNCLASSIFIED	1038
6184	18593385 (15727, 15728)			UNCLASSIFIED	1008
6185	49515548 (15733, 15734)			UNCLASSIFIED	1036
6186	15010520 (15735, 15736)			UNCLASSIFIED	1001
6187	79176937 (15739, 15740)			UNCLASSIFIED	1001
6188	65504551 (15741, 15742)			UNCLASSIFIED	1016
6189	55504307 (15751, 15752)			UNCLASSIFIED	1021

6190	35128137 (15755, 15756)			UNCLASSIFIED	1012
6191	29361307 (15757, 15758)			UNCLASSIFIED	1023
6192	23290193 (15769, 15770)			UNCLASSIFIED	1003
6193	65706368 (15771, 15772)			UNCLASSIFIED	1038
6194	39733782 (15785, 15786)			UNCLASSIFIED	1026
6195	82097441 (15799, 15800)			UNCLASSIFIED	1016, 1024, 1038
6196	55267313 (15819, 15820)			UNCLASSIFIED	1054
6197	80050089 (15821, 15822)			UNCLASSIFIED	1010
6198	54995300 (15823, 15824)			UNCLASSIFIED	1029
6199	87453862 (15825, 15826)			UNCLASSIFIED	1025
6200	11805874 (15827, 15828)			UNCLASSIFIED	1022
6201	71755047 (15845, 15846)			UNCLASSIFIED	1009
6202	79863766 (15861, 15862)			UNCLASSIFIED	1017
6203	57568192 (15863, 15864)			UNCLASSIFIED	1054
6204	66173638 (15885, 15886)			UNCLASSIFIED	1016
6205	77684257 (15909, 15910)			UNCLASSIFIED	1016
6206	65645917 (15921, 15922)			UNCLASSIFIED	1041
6207	13506310 (15933, 15934)			UNCLASSIFIED	1034

6208	79623652 (15947, 15948)			UNCLASSIFIED	1006, 1010, 1022, 1031
6209	79260126 (15951, 15952)			UNCLASSIFIED	1024
6210	46571816 (15953, 15954)			UNCLASSIFIED	1029
6211	28775980 (15981, 15982)			UNCLASSIFIED	1008
6212	13517784 (15993, 15994)			UNCLASSIFIED	1024
6213	79628916 (16011, 16012)			UNCLASSIFIED	1034, 1039
6214	70975001 (16013, 16014)			UNCLASSIFIED	1023
6215	91234901 (16015, 16016)			UNCLASSIFIED	1010
6216	20076720 (16017, 16018)			UNCLASSIFIED	1006, 1054
6217	25261451 (16057, 16058)			UNCLASSIFIED	1008
6218	11399510 (16063, 16064)			UNCLASSIFIED	1006
6219	94238214 (16067, 16068)			UNCLASSIFIED	1010
6220	12925720 (16097, 16098)			UNCLASSIFIED	1024
6221	17941867 (16107, 16108)			UNCLASSIFIED	1038
6222	29446961 (16133, 16134)			UNCLASSIFIED	1026
6223	80054226 (16145, 16146)			UNCLASSIFIED	1004
6224	30676527 (16155, 16156)			UNCLASSIFIED	1030
6225	65861723 (16173, 16174)			UNCLASSIFIED	1016

6226	20221778 (16191, 16192)			UNCLASSIFIED	1034
6227	78251017 (16209, 16210)			UNCLASSIFIED	1026
6228	65674666 (16213, 16214)			UNCLASSIFIED	1038
6229	27347859 (16215, 16216)			UNCLASSIFIED	1022
6230	32127312 (16217, 16218)			UNCLASSIFIED	1029
6231	65903183 (16221, 16222)			UNCLASSIFIED	1023
6232	78937123 (16223, 16224)			UNCLASSIFIED	1017, 1038
6233	49586655 (16237, 16238)			UNCLASSIFIED	1036
6234	95357326 (16251, 16252)			UNCLASSIFIED	1054
6235	78062993 (16257, 16258)			UNCLASSIFIED	1001
6236	80180274 (16265, 16266)			UNCLASSIFIED	1000, 1022
6237	20473985 (16275, 16276)			UNCLASSIFIED	1004, 1010
6238	99280757 (16281, 16282)			UNCLASSIFIED	1001, 1010
6239	39727970 (16287, 16288)			UNCLASSIFIED	1026
6240	65869753 (16295, 16296)			UNCLASSIFIED	1016
6241	58092972 (16305, 16306)			UNCLASSIFIED	1024
6242	66770570 (16317, 16318)			UNCLASSIFIED	1023, 1049
6243	78687480 (16321, 16322)			UNCLASSIFIED	1024

6244	34408083 (16325, 16326)			UNCLASSIFIED	1026
6245	66002234 (16329, 16330)			UNCLASSIFIED	1010, 1054
6246	79912122 (16337, 16338)			UNCLASSIFIED	1017
6247	79476974 (16351, 16352)			UNCLASSIFIED	1025
6248	11690067 (16367, 16368)			UNCLASSIFIED	1034
6249	19885930 (16369, 16370)			UNCLASSIFIED	1001, 1004
6250	28368014 (16377, 16378)			UNCLASSIFIED	1024
6251	80209869 (16381, 16382)			UNCLASSIFIED	1003, 1004, 1017, 1022, 1044
6252	65877778 (16387, 16388)			UNCLASSIFIED	1038
6253	34409804 (16397, 16398)			UNCLASSIFIED	1026
6254	82491768 (16407, 16408)			UNCLASSIFIED	1003, 1010, 1029
6255	39523348 (16409, 16410)			UNCLASSIFIED	1022, 1024
6256	23308540 (16411, 16412)			UNCLASSIFIED	1053
6257	48609584 (16419, 16420)			UNCLASSIFIED	1036
6258	79927771 (16427, 16428)			UNCLASSIFIED	1039
6259	78762359 (16431, 16432)			UNCLASSIFIED	1017, 1053
6260	47652318 (16433, 16434)			UNCLASSIFIED	1029
6261	10883803 (16441, 16442)			UNCLASSIFIED	1031

6262	70975008 (16443, 16444)			UNCLASSIFIED	1023
6263	95416422 (16453, 16454)			UNCLASSIFIED	1001, 1003, 1004, 1006, 1012, 1017, 1029, 1034, 1038, 1054
6264	87458994 (16469, 16470)			UNCLASSIFIED	1018
6265	65852879 (16477, 16478)			UNCLASSIFIED	1038
6266	91226211 (16509, 16510)			UNCLASSIFIED	1013, 1020, 1053
6267	16390345 (16513, 16514)			UNCLASSIFIED	1030
6268	11077618 (16519, 16520)			UNCLASSIFIED	1024
6269	55773995 (16539, 16540)			UNCLASSIFIED	1042
6270	11811649 (16555, 16556)			UNCLASSIFIED	1025
6271	34891868 (16573, 16574)			UNCLASSIFIED	1050
6272	78677624 (16575, 16576)			UNCLASSIFIED	1008
6273	65506366 (16577, 16578)			UNCLASSIFIED	1016, 1021
6274	20267181 (16585, 16586)			UNCLASSIFIED	1034
6275	79976663 (16587, 16588)			UNCLASSIFIED	1039
6276	39373467 (16593, 16594)			UNCLASSIFIED	1022
6277	79399334 (16659, 16660)			UNCLASSIFIED	1024
6278	30260317 (16671, 16672)			UNCLASSIFIED	1008

6279	46875679 (16675, 16676)			UNCLASSIFIED	1000
6280	78674442 (16679, 16680)			UNCLASSIFIED	1022
6281	27980826 (16687, 16688)			UNCLASSIFIED	1006
6282	29672933 (16689, 16690)			UNCLASSIFIED	1030
6283	12992052 (16693, 16694)			UNCLASSIFIED	1031
6284	56516463 (16703, 16704)			UNCLASSIFIED	1019
6285	11703605 (16707, 16708)			UNCLASSIFIED	1038
6286	10856407 (16709, 16710)			UNCLASSIFIED	1001
6287	94319101 (16713, 16714)			UNCLASSIFIED	1010
6288	58094076 (16727, 16728)			UNCLASSIFIED	1054
6289	79483800 (16729, 16730)			UNCLASSIFIED	1038
6290	11707576 (16811, 16812)			UNCLASSIFIED	1038
6291	78943339 (16823, 16824)			UNCLASSIFIED	1038
6292	79647741 (16825, 16826)			UNCLASSIFIED	1038
6293	78978570 (16831, 16832)			UNCLASSIFIED	1016
6294	29024905 (16835, 16836)			UNCLASSIFIED	1017
6295	80062444 (16839, 16840)			UNCLASSIFIED	1010
6296	87890476 (16851, 16852)			UNCLASSIFIED	1015

6297	66053538 (16865, 16866)			UNCLASSIFIED	1008
6298	20467513 (16877, 16878)			UNCLASSIFIED	1010, 1024, 1034
6299	78256335 (16885, 16886)			UNCLASSIFIED	1012, 1034
6300	79578444 (16889, 16890)			UNCLASSIFIED	1006, 1034
6301	35606207 (16895, 16896)			UNCLASSIFIED	1053
6302	65651050 (16903, 16904)			UNCLASSIFIED	1054
6303	21426931 (16905, 16906)			UNCLASSIFIED	1022
6304	11092942 (16907, 16908)			UNCLASSIFIED	1053
6305	54540147 (16917, 16918)			UNCLASSIFIED	1041
6306	80085964 (16919, 16920)			UNCLASSIFIED	1054
6307	79421045 (16921, 16922)			UNCLASSIFIED	1006
6308	11753810 (16925, 16926)			UNCLASSIFIED	1025
6309	80435984 (16929, 16930)			UNCLASSIFIED	1008, 1038, 1054
6310	79319129 (16931, 16932)			UNCLASSIFIED	1006
6311	79642855 (16937, 16938)			UNCLASSIFIED	1016, 1023, 1026, 1054
6312	79556912 (16953, 16954)			UNCLASSIFIED	1023
6313	27851527 (16957, 16958)			UNCLASSIFIED	1022
6314	55407090 (16969, 16970)			UNCLASSIFIED	1021

6315	33701019 (16973, 16974)				UNCLASSIFIED	1026
6316	78962410 (16977, 16978)				UNCLASSIFIED	1022, 1044
6317	78315334 (16989, 16990)				UNCLASSIFIED	1026
6318	35106114 (16993, 16994)				UNCLASSIFIED	1026
6319	29501291 (16997, 16998)				UNCLASSIFIED	1038
6320	20263112 (17001, 17002)				UNCLASSIFIED	1034
6321	87115276 (17007, 17008)				UNCLASSIFIED	1025
6322	78400129 (17009, 17010)				UNCLASSIFIED	1038
6323	79261539 (17015, 17016)				UNCLASSIFIED	1024
6324	80586929 (17029, 17030)				UNCLASSIFIED	1058
6325	20385668 (17037, 17038)				UNCLASSIFIED	1004
6326	94321867 (17039, 17040)				UNCLASSIFIED	1003
6327	27961840 (17065, 17066)				UNCLASSIFIED	1022
6328	79452020 (17077, 17078)				UNCLASSIFIED	1024
6329	24124853 (17085, 17086)				UNCLASSIFIED	1044
6330	80478691 (17095, 17096)				UNCLASSIFIED	1006, 1010, 1012, 1024
6331	30197903 (17101, 17102)				UNCLASSIFIED	1026
6332	86464845 (17117, 17118)				UNCLASSIFIED	1029

6333	78170799 (17123, 17124)			UNCLASSIFIED	1022, 1042, 1050
6334	87114572 (17133, 17134)			UNCLASSIFIED	1025
6335	81854392 (17139, 17140)			UNCLASSIFIED	1054
6336	20446483 (17147, 17148)			UNCLASSIFIED	1024
6337	85809498 (17151, 17152)			UNCLASSIFIED	1048
6338	86467214 (17153, 17154)			UNCLASSIFIED	1029
6339	79921517 (17161, 17162)			UNCLASSIFIED	1003
6340	65460344 (17183, 17184)			UNCLASSIFIED	1054
6341	80048274 (17185, 17186)			UNCLASSIFIED	1004, 1034
6342	10140934 (17191, 17192)			UNCLASSIFIED	1025
6343	65474074 (17199, 17200)			UNCLASSIFIED	1038
6344	37034577 (17205, 17206)			UNCLASSIFIED	1012
6345	80035315 (17207, 17208)			UNCLASSIFIED	1053
6346	86686995 (17261, 17262)			UNCLASSIFIED	1019
6347	80159404 (17265, 17266)			UNCLASSIFIED	1008, 1022
6348	11804069 (17279, 17280)			UNCLASSIFIED	1006
6349	91226510 (17287, 17288)			UNCLASSIFIED	1010
6350	78086151 (17301, 17302)			UNCLASSIFIED	1033

6351	94319109 (17311, 17312)			UNCLASSIFIED	1010, 1022, 1023, 1039, 1044
6352	34871792 (17319, 17320)			UNCLASSIFIED	1029
6353	27844610 (17337, 17338)			UNCLASSIFIED	1022
6354	86665887 (17351, 17352)			UNCLASSIFIED	1048
6355	79963112 (17361, 17362)			UNCLASSIFIED	1034
6356	63706749 (17367, 17368)			UNCLASSIFIED	1038
6357	27923824 (17371, 17372)			UNCLASSIFIED	1006
6358	80029712 (17383, 17384)			UNCLASSIFIED	1006, 1017, 1025
6359	20296403 (17407, 17408)			UNCLASSIFIED	1034
6360	78734259 (17419, 17420)			UNCLASSIFIED	1030
6361	79650090 (17425, 17426)			UNCLASSIFIED	1024, 1038
6362	8374659 (17429, 17430)			UNCLASSIFIED	1010
6363	20711340 (17435, 17436)			UNCLASSIFIED	1006
6364	15540826 (17443, 17444)			UNCLASSIFIED	1038
6365	79206191 (17445, 17446)			UNCLASSIFIED	1034
6366	24121926 (17449, 17450)			UNCLASSIFIED	1003
6367	65652167 (17455, 17456)			UNCLASSIFIED	1054
6368	27843884 (17457, 17458)			UNCLASSIFIED	1022, 1034

6369	78491411 (17467, 17468)			UNCLASSIFIED	1030
6370	20292668 (17477, 17478)			UNCLASSIFIED	1034
6371	88329083 (17485, 17486)			UNCLASSIFIED	1058
6372	94240512 (17491, 17492)			UNCLASSIFIED	1039
6373	11698663 (17503, 17504)			UNCLASSIFIED	1034
6374	79613989 (17537, 17538)			UNCLASSIFIED	1034
6375	46805463 (17541, 17542)			UNCLASSIFIED	1034
6376	80241251 (17555, 17556)			UNCLASSIFIED	1006, 1024, 1030, 1054
6377	78462469 (17567, 17568)			UNCLASSIFIED	1008
6378	10881403 (17601, 17602)			UNCLASSIFIED	1016
6379	91228184 (17621, 17622)			UNCLASSIFIED	1010
6380	32126348 (17625, 17626)			UNCLASSIFIED	1008
6381	57764348 (17631, 17632)			UNCLASSIFIED	1022
6382	46571821 (17645, 17646)			UNCLASSIFIED	1029
6383	97983610 (17661, 17662)			UNCLASSIFIED	1031
6384	79778528 (17667, 17668)			UNCLASSIFIED	1017
6385	65467432 (17675, 17676)			UNCLASSIFIED	1054
6386	65479198 (17689, 17690)			UNCLASSIFIED	1054

6387	25265657 (17705, 17706)			UNCLASSIFIED	1023
6388	13086093 (17707, 17708)			UNCLASSIFIED	1027
6389	80084307 (17709, 17710)			UNCLASSIFIED	1004, 1009, 1022, 1034
6390	11388460 (17717, 17718)			UNCLASSIFIED	1034
6391	94239442 (17733, 17734)			UNCLASSIFIED	1054
6392	28400359 (17745, 17746)			UNCLASSIFIED	1023
6393	78785225 (17753, 17754)			UNCLASSIFIED	1022
6394	79777158 (17769, 17770)			UNCLASSIFIED	1008, 1017, 1044
6395	23209563 (17781, 17782)			UNCLASSIFIED	1003
6396	77800216 (17785, 17786)			UNCLASSIFIED	1016, 1038, 1049
6397	79551380 (17793, 17794)			UNCLASSIFIED	1016, 1038
6398	65484487 (17795, 17796)			UNCLASSIFIED	1038
6399	34122592 (17805, 17806)			UNCLASSIFIED	1050
6400	38339218 (17815, 17816)			UNCLASSIFIED	1008
6401	39570371 (17819, 17820)			UNCLASSIFIED	1024
6402	79241990 (17835, 17836)			UNCLASSIFIED	1003, 1006, 1016, 1022, 1024, 1044
6403	79626037 (17839, 17840)			UNCLASSIFIED	1038
6404	78733552 (17883, 17884)			UNCLASSIFIED	1022, 1023

6405	49315616 (17885, 17886)			UNCLASSIFIED	1036
6406	19880144 (17897, 17898)			UNCLASSIFIED	1034
6407	78753782 (17903, 17904)			UNCLASSIFIED	1003, 1029, 1053
6408	11688804 (17905, 17906)			UNCLASSIFIED	1022
6409	20456456 (17909, 17910)			UNCLASSIFIED	1010
6410	24132224 (17917, 17918)			UNCLASSIFIED	1003
6411	85513355 (17935, 17936)			UNCLASSIFIED	1049
6412	79486655 (17957, 17958)			UNCLASSIFIED	1038
6413	10141070 (17973, 17974)			UNCLASSIFIED	1016
6414	65680368 (17975, 17976)			UNCLASSIFIED	1010
6415	71058581 (17977, 17978)			UNCLASSIFIED	1024
6416	20472005 (17981, 17982)			UNCLASSIFIED	1022
6417	78503004 (17993, 17994)			UNCLASSIFIED	1026
6418	78767700 (18013, 18014)			UNCLASSIFIED	1008
6419	11399525 (18023, 18024)			UNCLASSIFIED	1006
6420	94989431 (18039, 18040)			UNCLASSIFIED	1058
6421	7977766 (18045, 18046)			UNCLASSIFIED	1001, 1008, 1017
6422	78377873 (18061, 18062)			UNCLASSIFIED	1026

6423	80213899 (18063, 18064)			UNCLASSIFIED	1004, 1053
6424	21393716 (18073, 18074)			UNCLASSIFIED	1024
6425	20446839 (18081, 18082)			UNCLASSIFIED	1024
6426	78466176 (18097, 18098)			UNCLASSIFIED	1026
6427	95085670 (18105, 18106)			UNCLASSIFIED	1010
6428	79833809 (18107, 18108)			UNCLASSIFIED	1008
6429	66391698 (18117, 18118)			UNCLASSIFIED	1003, 1004, 1016, 1040
6430	95354078 (18153, 18154)			UNCLASSIFIED	1010, 1024
6431	17657563 (18157, 18158)			UNCLASSIFIED	1017
6432	66253062 (18159, 18160)			UNCLASSIFIED	1016
6433	30579725 (18171, 18172)			UNCLASSIFIED	1009
6434	78984145 (18179, 18180)			UNCLASSIFIED	1008
6435	11688384 (18183, 18184)			UNCLASSIFIED	1031
6436	33765151 (18223, 18224)			UNCLASSIFIED	1026
6437	65697756 (18251, 18252)			UNCLASSIFIED	1037, 1038
6438	28358389 (18253, 18254)			UNCLASSIFIED	1054
6439	65445206 (18255, 18256)			UNCLASSIFIED	1016
6440	20583996 (18257, 18258)			UNCLASSIFIED	1022

6441	95196834 (18263, 18264)			UNCLASSIFIED	1054
6442	79477438 (18269, 18270)			UNCLASSIFIED	1038
6443	80093172 (18271, 18272)			UNCLASSIFIED	1023, 1024
6444	88095537 (18277, 18278)			UNCLASSIFIED	1001, 1003, 1006, 1008, 1034, 1044, 1054
6445	98959418 (18279, 18280)			UNCLASSIFIED	1003, 1010, 1044
6446	78799070 (18301, 18302)			UNCLASSIFIED	1026
6447	86381161 (18323, 18324)			UNCLASSIFIED	1053
6448	77968376 (18325, 18326)			UNCLASSIFIED	1054
6449	10053042 (18331, 18332)			UNCLASSIFIED	1044
6450	86684218 (18337, 18338)			UNCLASSIFIED	1029
6451	79864292 (18339, 18340)			UNCLASSIFIED	1001, 1038
6452	70620612 (18343, 18344)			UNCLASSIFIED	1036, 1042
6453	58092806 (18351, 18352)			UNCLASSIFIED	1038
6454	32426883 (18355, 18356)			UNCLASSIFIED	1038
6455	11768574 (18359, 18360)			UNCLASSIFIED	1038
6456	86477505 (18365, 18366)			UNCLASSIFIED	1029
6457	10327238 (18369, 18370)			UNCLASSIFIED	1038
6458	78674662 (18393, 18394)			UNCLASSIFIED	1022

6459	79175833 (18397, 18398)			UNCLASSIFIED	1024
6460	46803653 (18411, 18412)			UNCLASSIFIED	1001
6461	78369480 (18413, 18414)			UNCLASSIFIED	1003
6462	37028955 (18423, 18424)			UNCLASSIFIED	1038
6463	78727258 (18425, 18426)			UNCLASSIFIED	1030
6464	38070037 (18439, 18440)			UNCLASSIFIED	1016
6465	15019257 (18441, 18442)			UNCLASSIFIED	1053
6466	39562008 (18443, 18444)			UNCLASSIFIED	1022
6467	77805342 (18479, 18480)			UNCLASSIFIED	1022
6468	80578631 (18485, 18486)			UNCLASSIFIED	1058
6469	79329498 (18487, 18488)			UNCLASSIFIED	1053
6470	30248596 (18495, 18496)			UNCLASSIFIED	1026
6471	78164304 (18499, 18500)			UNCLASSIFIED	1030
6472	65863790 (18507, 18508)			UNCLASSIFIED	1016
6473	65453754 (18531, 18532)			UNCLASSIFIED	1016
6474	79868333 (18545, 18546)			UNCLASSIFIED	1012
6475	94136642 (18547, 18548)			UNCLASSIFIED	1003
6476	42940779 (18583, 18584)			UNCLASSIFIED	1037

6477	21412682 (18591, 18592)			UNCLASSIFIED	1004
6478	17941878 (18601, 18602)			UNCLASSIFIED	1008
6479	78374913 (18613, 18614)			UNCLASSIFIED	1003
6480	98426268 (18641, 18642)			UNCLASSIFIED	1010, 1016, 1038, 1040, 1054
6481	78461448 (18643, 18644)			UNCLASSIFIED	1026
6482	27296166 (18663, 18664)			UNCLASSIFIED	1009
6483	33744053 (18675, 18676)			UNCLASSIFIED	1016
6484	78761449 (18677, 18678)			UNCLASSIFIED	1030
6485	27842029 (18681, 18682)			UNCLASSIFIED	1022
6486	30175490 (18691, 18692)			UNCLASSIFIED	1006, 1008
6487	78085399 (18697, 18698)			UNCLASSIFIED	1037
6488	78146641 (18717, 18718)			UNCLASSIFIED	1026
6489	65896710 (18725, 18726)			UNCLASSIFIED	1022, 1054
6490	20297577 (18733, 18734)			UNCLASSIFIED	1034
6491	80501488 (18747, 18748)			UNCLASSIFIED	1012, 1024
6492	78959091 (18781, 18782)			UNCLASSIFIED	1008, 1009, 1039
6493	87890939 (18785, 18786)			UNCLASSIFIED	1015, 1025
6494	29471220 (18795, 18796)			UNCLASSIFIED	1022

6495	29690767 (18797, 18798)			UNCLASSIFIED	1016
6496	79973410 (18801, 18802)			UNCLASSIFIED	1034, 1054
6497	79756471 (18811, 18812)			UNCLASSIFIED	1004, 1022
6498	78029462 (18813, 18814)			UNCLASSIFIED	1008
6499	54599809 (18817, 18818)			UNCLASSIFIED	1041
6500	16316988 (18831, 18832)			UNCLASSIFIED	1001
6501	82053350 (18833, 18834)			UNCLASSIFIED	1006, 1012, 1016, 1034
6502	37004396 (18841, 18842)			UNCLASSIFIED	1029
6503	79863605 (18853, 18854)			UNCLASSIFIED	1038
6504	27964519 (18859, 18860)			UNCLASSIFIED	1034
6505	71838508 (18903, 18904)			UNCLASSIFIED	1030
6506	78268902 (18911, 18912)			UNCLASSIFIED	1024
6507	65681302 (18943, 18944)			UNCLASSIFIED	1041
6508	78789089 (18951, 18952)			UNCLASSIFIED	1008
6509	79873230 (18957, 18958)			UNCLASSIFIED	1003, 1017, 1034, 1054
6510	65894683 (18959, 18960)			UNCLASSIFIED	1016
6511	17882378 (18965, 18966)			UNCLASSIFIED	1039
6512	40382541 (18975, 18976)			UNCLASSIFIED	1037

6513	27843890 (18977, 18978)			UNCLASSIFIED	1010, 1012, 1022, 1031, 1034, 1039
6514	78901850 (18985, 18986)			UNCLASSIFIED	1039
6515	79764645 (18993, 18994)			UNCLASSIFIED	1001, 1003, 1008, 1024
6516	78892361 (18999, 19000)			UNCLASSIFIED	1017
6517	50887373 (19003, 19004)			UNCLASSIFIED	1036
6518	65658644 (19005, 19006)			UNCLASSIFIED	1054
6519	13417570 (19019, 19020)			UNCLASSIFIED	1027
6520	79763279 (19031, 19032)			UNCLASSIFIED	1008
6521	80385041 (19057, 19058)			UNCLASSIFIED	1029
6522	79558281 (19059, 19060)			UNCLASSIFIED	1038
6523	33202668 (19065, 19066)			UNCLASSIFIED	1026
6524	20297461 (19071, 19072)			UNCLASSIFIED	1034
6525	9849420 (19075, 19076)			UNCLASSIFIED	1008
6526	80477772 (19079, 19080)			UNCLASSIFIED	1012
6527	21416435 (19083, 19084)			UNCLASSIFIED	1022
6528	87453055 (19091, 19092)			UNCLASSIFIED	1025
6529	80067674 (19099, 19100)			UNCLASSIFIED	1010
6530	86477696 (19109, 19110)			UNCLASSIFIED	1029

6531	66694504 (19117, 19118)			UNCLASSIFIED	1049
6532	30158760 (19131, 19132)			UNCLASSIFIED	1006, 1008, 1022, 1024
6533	10869231 (19133, 19134)			UNCLASSIFIED	1024
6534	13000747 (19135, 19136)			UNCLASSIFIED	1024
6535	57461768 (19137, 19138)			UNCLASSIFIED	1011
6536	78713835 (19139, 19140)			UNCLASSIFIED	1003
6537	94241436 (19141, 19142)			UNCLASSIFIED	1044
6538	19496580 (19145, 19146)			UNCLASSIFIED	1001
6539	81758497 (19151, 19152)			UNCLASSIFIED	1003, 1008, 1016, 1017, 1022, 1023, 1024, 1026, 1038, 1039, 1044, 1054
6540	16842113 (19159, 19160)			UNCLASSIFIED	1001, 1012, 1023, 1027
6541	6298182 (19167, 19168)			UNCLASSIFIED	1058
6542	38885157 (19173, 19174)			UNCLASSIFIED	1012
6543	66367021 (19181, 19182)			UNCLASSIFIED	1053
6544	33207355 (19189, 19190)			UNCLASSIFIED	1026
6545	70149940 (19193, 19194)			UNCLASSIFIED	1001, 1008, 1012
6546	78922427 (19199, 19200)			UNCLASSIFIED	1039

6547	33188274 (19205, 19206)			UNCLASSIFIED	1026
6548	78893753 (19209, 19210)			UNCLASSIFIED	1029
6549	79912745 (19217, 19218)			UNCLASSIFIED	1025
6550	30192660 (19219, 19220)			UNCLASSIFIED	1008
6551	78475904 (19227, 19228)			UNCLASSIFIED	1003
6552	36856730 (19241, 19242)			UNCLASSIFIED	1016
6553	65455387 (19243, 19244)			UNCLASSIFIED	1016
6554	79966806 (19265, 19266)			UNCLASSIFIED	1054
6555	80082181 (19271, 19272)			UNCLASSIFIED	1001, 1006, 1008, 1012, 1022, 1024, 1031
6556	28836888 (19273, 19274)			UNCLASSIFIED	1026
6557	77884197 (19285, 19286)			UNCLASSIFIED	1021
6558	11310995 (19289, 19290)			UNCLASSIFIED	1034
6559	79551396 (19295, 19296)			UNCLASSIFIED	1025
6560	29009809 (19297, 19298)			UNCLASSIFIED	1008
6561	30251424 (19303, 19304)			UNCLASSIFIED	1044
6562	10089956 (19313, 19314)			UNCLASSIFIED	1017
6563	49955443 (19315, 19316)			UNCLASSIFIED	1036
6564	87463300 (19321, 19322)			UNCLASSIFIED	1025

6565	56154672 (19355, 19356)			UNCLASSIFIED	1021
6566	11073944 (19357, 19358)			UNCLASSIFIED	1006
6567	29232396 (19359, 19360)			UNCLASSIFIED	1008
6568	10879838 (19379, 19380)			UNCLASSIFIED	1004
6569	94667725 (19385, 19386)			UNCLASSIFIED	1017
6570	80401811 (19395, 19396)			UNCLASSIFIED	1001, 1004, 1023, 1024, 1029, 1034, 1038, 1039, 1054
6571	79864114 (19399, 19400)			UNCLASSIFIED	1012
6572	14223759 (19403, 19404)			UNCLASSIFIED	1050
6573	95292755 (19405, 19406)			UNCLASSIFIED	1024, 1039
6574	11796516 (19427, 19428)			UNCLASSIFIED	1016
6575	52561125 (19435, 19436)			UNCLASSIFIED	1017
6576	65703978 (19475, 19476)			UNCLASSIFIED	1038
6577	35140465 (19487, 19488)			UNCLASSIFIED	1050
6578	65700282 (19489, 19490)			UNCLASSIFIED	1038
6579	25235948 (19493, 19494)			UNCLASSIFIED	1003
6580	37034102 (19507, 19508)			UNCLASSIFIED	1012
6581	94143303 (19511, 19512)			UNCLASSIFIED	1003

6582	80241965 (19537, 19538)			UNCLASSIFIED	1022
6583	9404258 (19539, 19540)			UNCLASSIFIED	1044
6584	86475898 (19555, 19556)			UNCLASSIFIED	1029
6585	65663427 (19569, 19570)			UNCLASSIFIED	1053
6586	79245319 (19573, 19574)			UNCLASSIFIED	1024
6587	27248495 (19575, 19576)			UNCLASSIFIED	1026
6588	56154814 (19577, 19578)			UNCLASSIFIED	1021
6589	32118434 (19591, 19592)			UNCLASSIFIED	1000
6590	7512127 (19599, 19600)			UNCLASSIFIED	1034
6591	95350928 (19603, 19604)			UNCLASSIFIED	1010
6592	28380672 (19619, 19620)			UNCLASSIFIED	1008
6593	76376066 (19635, 19636)			UNCLASSIFIED	1026
6594	94134724 (19639, 19640)			UNCLASSIFIED	1010
6595	78288306 (19647, 19648)			UNCLASSIFIED	1029
6596	78484226 (19657, 19658)			UNCLASSIFIED	1026
6597	78523609 (19665, 19666)			UNCLASSIFIED	1006, 1008
6598	79480843 (19669, 19670)			UNCLASSIFIED	1038
6599	21425248 (19671, 19672)			UNCLASSIFIED	1022

6600	10144676 (19687, 19688)			UNCLASSIFIED	1025
6601	78192311 (19707, 19708)			UNCLASSIFIED	1009, 1038, 1054
6602	25133645 (19715, 19716)			UNCLASSIFIED	1003
6603	46866506 (19725, 19726)			UNCLASSIFIED	1037
6604	20456936 (19729, 19730)			UNCLASSIFIED	1010
6605	78912563 (19747, 19748)			UNCLASSIFIED	1039
6606	30539784 (19761, 19762)			UNCLASSIFIED	1026
6607	13516983 (19773, 19774)			UNCLASSIFIED	1024
6608	29686602 (19775, 19776)			UNCLASSIFIED	1009
6609	79633531 (19777, 19778)			UNCLASSIFIED	1038, 1039
6610	80239251 (19795, 19796)			UNCLASSIFIED	1022, 1034
6611	30787321 (19797, 19798)			UNCLASSIFIED	1001
6612	78742294 (19805, 19806)			UNCLASSIFIED	1044
6613	94326041 (19807, 19808)			UNCLASSIFIED	1044
6614	86462816 (19813, 19814)			UNCLASSIFIED	1007, 1042, 1048, 1050, 1054, 1057
6615	78770391 (19817, 19818)			UNCLASSIFIED	1017
6616	11420185 (19849, 19850)			UNCLASSIFIED	1017
6617	55409202 (19853, 19854)			UNCLASSIFIED	1021

6618	65883637 (19855, 19856)			UNCLASSIFIED	1053, 1054
6619	91237376 (19867, 19868)			UNCLASSIFIED	1045
6620	66770598 (19871, 19872)			UNCLASSIFIED	1010, 1049
6621	17940450 (19877, 19878)			UNCLASSIFIED	1039
6622	78031938 (19901, 19902)			UNCLASSIFIED	1024
6623	25260233 (19905, 19906)			UNCLASSIFIED	1008
6624	78483658 (19909, 19910)			UNCLASSIFIED	1026
6625	37011892 (19917, 19918)			UNCLASSIFIED	1029
6626	77722402 (19919, 19920)			UNCLASSIFIED	1054
6627	30271044 (19923, 19924)			UNCLASSIFIED	1026
6628	20456147 (19925, 19926)			UNCLASSIFIED	1010
6629	86684742 (19929, 19930)			UNCLASSIFIED	1029
6630	78185541 (19959, 19960)			UNCLASSIFIED	1029, 1055
6631	65868558 (19961, 19962)			UNCLASSIFIED	1006, 1024
6632	36996119 (19963, 19964)			UNCLASSIFIED	1001
6633	83743633 (19973, 19974)			UNCLASSIFIED	1053
6634	28086352 (19979, 19980)			UNCLASSIFIED	1003
6635	65697938 (20009, 20010)			UNCLASSIFIED	1024, 1038

6636	19880155 (20011, 20012)			UNCLASSIFIED	1034
6637	79549290 (20023, 20024)			UNCLASSIFIED	1025
6638	80423054 (20025, 20026)			UNCLASSIFIED	1017, 1022, 1024, 1025
6639	10881223 (20049, 20050)			UNCLASSIFIED	1025
6640	66254631 (20059, 20060)			UNCLASSIFIED	1016
6641	11130341 (20063, 20064)			UNCLASSIFIED	1004
6642	94665090 (20075, 20076)			UNCLASSIFIED	1024
6643	29357909 (20077, 20078)			UNCLASSIFIED	1022
6644	14999618 (20109, 20110)			UNCLASSIFIED	1027
6645	11424294 (20111, 20112)			UNCLASSIFIED	1017
6646	65985592 (20115, 20116)			UNCLASSIFIED	1054
6647	85800760 (20117, 20118)			UNCLASSIFIED	1025
6648	55180236 (20125, 20126)			UNCLASSIFIED	1019
6649	85528662 (20127, 20128)			UNCLASSIFIED	1038
6650	21650745 (20135, 20136)			UNCLASSIFIED	1044
6651	78985325 (20161, 20162)			UNCLASSIFIED	1017, 1022
6652	79193648 (20163, 20164)			UNCLASSIFIED	1024
6653	80246711 (20169, 20170)			UNCLASSIFIED	1017, 1053

6654	79957653 (20175, 20176)			UNCLASSIFIED	1017
6655	80053285 (20177, 20178)			UNCLASSIFIED	1004, 1024, 1038
6656	87458132 (20179, 20180)			UNCLASSIFIED	1018
6657	78946560 (20191, 20192)			UNCLASSIFIED	1054
6658	17294320 (20193, 20194)			UNCLASSIFIED	1039
6659	95085689 (20225, 20226)			UNCLASSIFIED	1003
6660	11771339 (20239, 20240)			UNCLASSIFIED	1031
6661	16374631 (20259, 20260)			UNCLASSIFIED	1022, 1023
6662	81885897 (20279, 20280)			UNCLASSIFIED	1004, 1029, 1054
6663	79967464 (20289, 20290)			UNCLASSIFIED	1034
6664	21632244 (20313, 20314)			UNCLASSIFIED	1006
6665	79411433 (20317, 20318)			UNCLASSIFIED	1024
6666	80427583 (20319, 20320)			UNCLASSIFIED	1023, 1025
6667	80021433 (20325, 20326)			UNCLASSIFIED	1022
6668	87913201 (20329, 20330)			UNCLASSIFIED	1016, 1018, 1022
6669	80025276 (20337, 20338)			UNCLASSIFIED	1004
6670	70287218 (20353, 20354)			UNCLASSIFIED	1009
6671	95358370 (20375, 20376)			UNCLASSIFIED	1058

6672	78685667 (20391, 20392)			UNCLASSIFIED	1017, 1025
6673	30537259 (20399, 20400)			UNCLASSIFIED	1026
6674	46849809 (20401, 20402)			UNCLASSIFIED	1029
6675	65501280 (20411, 20412)			UNCLASSIFIED	1016
6676	79759546 (20413, 20414)			UNCLASSIFIED	1003, 1022, 1023, 1029, 1031, 1053
6677	66556266 (20441, 20442)			UNCLASSIFIED	1023, 1029
6678	71846535 (20449, 20450)			UNCLASSIFIED	1016, 1019, 1038
6679	51621152 (20453, 20454)			UNCLASSIFIED	1036
6680	65897693 (20467, 20468)			UNCLASSIFIED	1016, 1023
6681	10881006 (20479, 20480)			UNCLASSIFIED	1038
6682	30197925 (20493, 20494)			UNCLASSIFIED	1026
6683	30270530 (20501, 20502)			UNCLASSIFIED	1008
6684	27976166 (20519, 20520)			UNCLASSIFIED	1053
6685	5640845 (20521, 20522)			UNCLASSIFIED	1068
6686	20297948 (20531, 20532)			UNCLASSIFIED	1034
6687	35051908 (20533, 20534)			UNCLASSIFIED	1022
6688	54701630 (20535, 20536)			UNCLASSIFIED	1036, 1054
6689	98220400 (20541, 20542)			UNCLASSIFIED	1006, 1030, 1044

6690	66468057 (20543, 20544)			UNCLASSIFIED	1024
6691	23329744 (20553, 20554)			UNCLASSIFIED	1026
6692	11694506 (20557, 20558)			UNCLASSIFIED	1001, 1034
6693	87453892 (20565, 20566)			UNCLASSIFIED	1007, 1025
6694	77879679 (20581, 20582)			UNCLASSIFIED	1019
6695	56072833 (20585, 20586)			UNCLASSIFIED	1009
6696	11083944 (20599, 20600)			UNCLASSIFIED	1024
6697	33202122 (20601, 20602)			UNCLASSIFIED	1026
6698	29350591 (20619, 20620)			UNCLASSIFIED	1017
6699	21434972 (20643, 20644)			UNCLASSIFIED	1024
6700	10102678 (20647, 20648)			UNCLASSIFIED	1012
6701	79825444 (20653, 20654)			UNCLASSIFIED	1044
6702	80398431 (20669, 20670)			UNCLASSIFIED	1008, 1029
6703	20292156 (20709, 20710)			UNCLASSIFIED	1034
6704	77588735 (20743, 20744)			UNCLASSIFIED	1049
6705	20623835 (20745, 20746)			UNCLASSIFIED	1004
6706	5286465 (20759, 20760)			UNCLASSIFIED	1058
6707	78952370 (20767, 20768)			UNCLASSIFIED	1016

6708	54527124 (20783, 20784)			UNCLASSIFIED	1041
6709	66173662 (20789, 20790)			UNCLASSIFIED	1016
6710	71109596 (20815, 20816)			UNCLASSIFIED	1029
6711	20615659 (20835, 20836)			UNCLASSIFIED	1004
6712	80248179 (20853, 20854)			UNCLASSIFIED	1006
6713	7700013 (20857, 20858)			UNCLASSIFIED	1012, 1034
6714	46890237 (20863, 20864)			UNCLASSIFIED	1019
6715	79911071 (20875, 20876)			UNCLASSIFIED	1038
6716	95292765 (20877, 20878)			UNCLASSIFIED	1006, 1024
6717	16738239 (20879, 20880)			UNCLASSIFIED	1017
6718	78925093 (20881, 20882)			UNCLASSIFIED	1054
6719	10237137 (20899, 20900)			UNCLASSIFIED	1039
6720	54966864 (20915, 20916)			UNCLASSIFIED	1037
6721	55184965 (20923, 20924)			UNCLASSIFIED	1037
6722	80260582 (20925, 20926)			UNCLASSIFIED	1024, 1034
6723	37003564 (20949, 20950)			UNCLASSIFIED	1029
6724	30650728 (20965, 20966)			UNCLASSIFIED	1008
6725	25256741 (20967, 20968)			UNCLASSIFIED	1003

6726	77694079 (21005, 21006)			UNCLASSIFIED	1004
6727	28489322 (21041, 21042)			UNCLASSIFIED	1022
6728	65507911 (21043, 21044)			UNCLASSIFIED	1038
6729	46874732 (21045, 21046)			UNCLASSIFIED	1050
6730	25241134 (21051, 21052)			UNCLASSIFIED	1039
6731	78394531 (21075, 21076)			UNCLASSIFIED	1030
6732	65487012 (21083, 21084)			UNCLASSIFIED	1023
6733	13084204 (21091, 21092)			UNCLASSIFIED	1024
6734	85525183 (21093, 21094)			UNCLASSIFIED	1038
6735	65704703 (21095, 21096)			UNCLASSIFIED	1041
6736	90938262 (21097, 21098)			UNCLASSIFIED	1020
6737	65861758 (21107, 21108)			UNCLASSIFIED	1008, 1016, 1023, 1024, 1038, 1039, 1044, 1054
6738	20377410 (21109, 21110)			UNCLASSIFIED	1010
6739	12966947 (21113, 21114)			UNCLASSIFIED	1031
6740	85811480 (21121, 21122)			UNCLASSIFIED	1019, 1054
6741	79242591 (21123, 21124)			UNCLASSIFIED	1039
6742	27849426 (21133, 21134)			UNCLASSIFIED	1010

6743	71471627 (21135, 21136)			UNCLASSIFIED	1000, 1024
6744	78511360 (21153, 21154)			UNCLASSIFIED	1054
6745	20724462 (21155, 21156)			UNCLASSIFIED	1006
6746	80257730 (21167, 21168)			UNCLASSIFIED	1022
6747	86667153 (21175, 21176)			UNCLASSIFIED	1029
6748	79634678 (21179, 21180)			UNCLASSIFIED	1023
6749	10185459 (21183, 21184)			UNCLASSIFIED	1003
6750	25322622 (21201, 21202)			UNCLASSIFIED	1008
6751	78928316 (21203, 21204)			UNCLASSIFIED	1017
6752	79561719 (21217, 21218)			UNCLASSIFIED	1044
6753	66028187 (21219, 21220)			UNCLASSIFIED	1003
6754	32116053 (21253, 21254)			UNCLASSIFIED	1026
6755	77520607 (21261, 21262)			UNCLASSIFIED	1049
6756	88094992 (21283, 21284)			UNCLASSIFIED	1010
6757	79846109 (21293, 21294)			UNCLASSIFIED	1034
6758	79600110 (21295, 21296)			UNCLASSIFIED	1039
6759	27355032 (21303, 21304)			UNCLASSIFIED	1003, 1009, 1027, 1034
6760	28473542 (21343, 21344)			UNCLASSIFIED	1030

6761	25322022 (21347, 21348)			UNCLASSIFIED	1009
6762	27980692 (21349, 21350)			UNCLASSIFIED	1006
6763	30158944 (21355, 21356)			UNCLASSIFIED	1029
6764	79484876 (21359, 21360)			UNCLASSIFIED	1034
6765	20449712 (21365, 21366)			UNCLASSIFIED	1022
6766	35061023 (21371, 21372)			UNCLASSIFIED	1054
6767	27976768 (21377, 21378)			UNCLASSIFIED	1022
6768	19756458 (21387, 21388)			UNCLASSIFIED	1023
6769	78495735 (21403, 21404)			UNCLASSIFIED	1038
6770	79604896 (21409, 21410)			UNCLASSIFIED	1039
6771	46801655 (21443, 21444)			UNCLASSIFIED	1054
6772	65978245 (21447, 21448)			UNCLASSIFIED	1054
6773	19631304 (21459, 21460)			UNCLASSIFIED	1054
6774	25260854 (21465, 21466)			UNCLASSIFIED	1026
6775	65703829 (21479, 21480)			UNCLASSIFIED	1038
6776	23304348 (21483, 21484)			UNCLASSIFIED	1023
6777	20708154 (21491, 21492)			UNCLASSIFIED	1006
6778	78405682 (21493, 21494)			UNCLASSIFIED	1016

6779	7521054 (21503, 21504)			UNCLASSIFIED	1058
6780	11071108 (21507, 21508)			UNCLASSIFIED	1034
6781	47652347 (21525, 21526)			UNCLASSIFIED	1029
6782	71820936 (21541, 21542)			UNCLASSIFIED	1008
6783	87112435 (21545, 21546)			UNCLASSIFIED	1008, 1034, 1038
6784	11347036 (21549, 21550)			UNCLASSIFIED	1022
6785	79841410 (21557, 21558)			UNCLASSIFIED	1038
6786	37419704 (21559, 21560)			UNCLASSIFIED	1016
6787	10370047 (21563, 21564)			UNCLASSIFIED	1017
6788	33455235 (21568, 21570)			UNCLASSIFIED	1029
6789	33764191 (21571, 21572)			UNCLASSIFIED	1026
6790	85800326 (21573, 21574)			UNCLASSIFIED	1025
6791	20140426 (21585, 21586)			UNCLASSIFIED	1034
6792	30535406 (21595, 21596)			UNCLASSIFIED	1026
6793	16424745 (21597, 21598)			UNCLASSIFIED	1038
6794	54701036 (21629, 21630)			UNCLASSIFIED	1019
6795	20620764 (21637, 21638)			UNCLASSIFIED	1034
6796	21639344 (21655, 21656)			UNCLASSIFIED	1017

6797	24128820 (21681, 21682)			UNCLASSIFIED	1003, 1022
6798	10159618 (21685, 21686)			UNCLASSIFIED	1001
6799	23289970 (21689, 21690)			UNCLASSIFIED	1044
6800	32734844 (21703, 21704)			UNCLASSIFIED	1001
6801	78369035 (21711, 21712)			UNCLASSIFIED	1017
6802	65902412 (21715, 21716)			UNCLASSIFIED	1023
6803	94233902 (21723, 21724)			UNCLASSIFIED	1003, 1023
6804	20691310 (21739, 21740)			UNCLASSIFIED	1010
6805	77801513 (21757, 21758)			UNCLASSIFIED	1024, 1049
6806	70945161 (21759, 21760)			UNCLASSIFIED	1029, 1057
6807	28461558 (21761, 21762)			UNCLASSIFIED	1003
6808	85822907 (21777, 21778)			UNCLASSIFIED	1048
6809	79834932 (21807, 21808)			UNCLASSIFIED	1022, 1039
6810	79918164 (21811, 21812)			UNCLASSIFIED	1039
6811	33267551 (21819, 21820)			UNCLASSIFIED	1001
6812	56317846 (21825, 21826)			UNCLASSIFIED	1008
6813	21659280 (21843, 21844)			UNCLASSIFIED	1034
6814	25140461 (21853, 21854)			UNCLASSIFIED	1026

6815	28457374 (21859, 21860)			UNCLASSIFIED	1023
6816	94321093 (21869, 21870)			UNCLASSIFIED	1003
6817	82301988 (21913, 21914)			UNCLASSIFIED	1001, 1053
6818	57118716 (21939, 21940)			UNCLASSIFIED	1054
6819	20182667 (21957, 21958)			UNCLASSIFIED	1010
6820	37060658 (21959, 21960)			UNCLASSIFIED	1054
6821	80243243 (21975, 21976)			UNCLASSIFIED	1016, 1022, 1026, 1030, 1038
6822	35137780 (21983, 21984)			UNCLASSIFIED	1050
6823	78392279 (21993, 21994)			UNCLASSIFIED	1038
6824	11694826 (21997, 21998)			UNCLASSIFIED	1038
6825	11362222 (22001, 22002)			UNCLASSIFIED	1024
6826	65470256 (22019, 22020)			UNCLASSIFIED	1038
6827	34123703 (22023, 22024)			UNCLASSIFIED	1050
6828	54992964 (22033, 22034)			UNCLASSIFIED	1029
6829	58093604 (22037, 22038)			UNCLASSIFIED	1054
6830	13524050 (22039, 22040)			UNCLASSIFIED	1034
6831	80475452 (22045, 22046)			UNCLASSIFIED	1012, 1034, 1053
6832	11011875 (22057, 22058)			UNCLASSIFIED	1024

6833	20614211 (22061, 22062)			UNCLASSIFIED	1022
6834	58090346 (22065, 22066)			UNCLASSIFIED	1054
6835	66028348 (22071, 22072)			UNCLASSIFIED	1003
6836	27973133 (22075, 22076)			UNCLASSIFIED	1053
6837	78958511 (22077, 22078)			UNCLASSIFIED	1008
6838	28849319 (22083, 22084)			UNCLASSIFIED	1026
6839	28386703 (22085, 22086)			UNCLASSIFIED	1024
6840	20441371 (22087, 22088)			UNCLASSIFIED	1024
6841	32309249 (22097, 22098)			UNCLASSIFIED	1029
6842	69931298 (22099, 22100)			UNCLASSIFIED	1049
6843	80500092 (22101, 22102)			UNCLASSIFIED	1003, 1004, 1006, 1008, 1012, 1017, 1022, 1023, 1024, 1025, 1034, 1039, 1044, 1054
6844	13527909 (22105, 22106)			UNCLASSIFIED	1054
6845	47652190 (22109, 22110)			UNCLASSIFIED	1029
6846	27372003 (22111, 22112)			UNCLASSIFIED	1026
6847	78381424 (22113, 22114)			UNCLASSIFIED	1008, 1026, 1029, 1053
6848	79832196 (22117, 22118)			UNCLASSIFIED	1008, 1009, 1023

6849	65468206 (22133, 22134)			UNCLASSIFIED	1054
6850	95292778 (22149, 22150)			UNCLASSIFIED	1003, 1008, 1019, 1023, 1024, 1029
6851	66257954 (22157, 22158)			UNCLASSIFIED	1038
6852	27365648 (22159, 22160)			UNCLASSIFIED	1017
6853	20417133 (22161, 22162)			UNCLASSIFIED	1010
6854	77689889 (22165, 22166)			UNCLASSIFIED	1053
6855	29358969 (22167, 22168)			UNCLASSIFIED	1022
6856	79640646 (22177, 22178)			UNCLASSIFIED	1039
6857	24144678 (22179, 22180)			UNCLASSIFIED	1053
6858	80033045 (22187, 22188)			UNCLASSIFIED	1053
6859	77892413 (22203, 22204)			UNCLASSIFIED	1036
6860	95290415 (22221, 22222)			UNCLASSIFIED	1022
6861	11690923 (22233, 22234)			UNCLASSIFIED	1034
6862	78675379 (22245, 22246)			UNCLASSIFIED	1008
6863	46875341 (22273, 22274)			UNCLASSIFIED	1037
6864	94989451 (22285, 22286)			UNCLASSIFIED	1058
6865	71308289 (22313, 22314)			UNCLASSIFIED	1001
6866	57506772 (22317, 22318)			UNCLASSIFIED	1030, 1054

6867	28386845 (22335, 22336)			UNCLASSIFIED	1017
6868	82125373 (22339, 22340)			UNCLASSIFIED	1003, 1008, 1010, 1012, 1016, 1017, 1024, 1025, 1038, 1039, 1044
6869	13089692 (22347, 22348)			UNCLASSIFIED	1027
6870	66051884 (22363, 22364)			UNCLASSIFIED	1023
6871	20287043 (22365, 22366)			UNCLASSIFIED	1022
6872	10316653 (22379, 22380)			UNCLASSIFIED	1025
6873	79254929 (22401, 22402)			UNCLASSIFIED	1054
6874	80505065 (22407, 22408)			UNCLASSIFIED	1012
6875	29026044 (22415, 22416)			UNCLASSIFIED	1008
6876	87463875 (22417, 22418)			UNCLASSIFIED	1018
6877	8227093 (22421, 22422)			UNCLASSIFIED	1022
6878	78519206 (22437, 22438)			UNCLASSIFIED	1003
6879	78762689 (22443, 22444)			UNCLASSIFIED	1030
6880	30784314 (22445, 22446)			UNCLASSIFIED	1003
6881	79439660 (22467, 22468)			UNCLASSIFIED	1034
6882	65897233 (22483, 22484)			UNCLASSIFIED	1016
6883	17707149 (22505, 22506)			UNCLASSIFIED	1017

6884	19636169 (22511, 22512)			UNCLASSIFIED	1004
6885	20429966 (22518, 22520)			UNCLASSIFIED	1004
6886	20623842 (22521, 22522)			UNCLASSIFIED	1024
6887	11309716 (22523, 22524)			UNCLASSIFIED	1010
6888	18514279 (22543, 22544)			UNCLASSIFIED	1010
6889	79877966 (22547, 22548)			UNCLASSIFIED	1025
6890	78749016 (22575, 22576)			UNCLASSIFIED	1017
6891	57049676 (22585, 22586)			UNCLASSIFIED	1009
6892	78762232 (22609, 22610)			UNCLASSIFIED	1019, 1024, 1039
6893	79183326 (22611, 22612)			UNCLASSIFIED	1001, 1003, 1024
6894	33188794 (22621, 22622)			UNCLASSIFIED	1026
6895	78244202 (22623, 22624)			UNCLASSIFIED	1017, 1026
6896	86685943 (22629, 22630)			UNCLASSIFIED	1029
6897	79169728 (22637, 22638)			UNCLASSIFIED	1024
6898	11304549 (22641, 22642)			UNCLASSIFIED	1024
6899	57301504 (22649, 22650)			UNCLASSIFIED	1004
6900	80428695 (22651, 22652)			UNCLASSIFIED	1008, 1022, 1038, 1039, 1049
6901	8520726 (22659, 22660)			UNCLASSIFIED	1024

6902	29006126 (22661, 22662)			UNCLASSIFIED	1017
6903	54539432 (22673, 22674)			UNCLASSIFIED	1040
6904	80092096 (22703, 22704)			UNCLASSIFIED	1034
6905	80022300 (22729, 22730)			UNCLASSIFIED	1004, 1029
6906	35598037 (22783, 22784)			UNCLASSIFIED	1024
6907	37011599 (22795, 22796)			UNCLASSIFIED	1029
6908	78761289 (22803, 22804)			UNCLASSIFIED	1008, 1026
6909	79116899 (22851, 22852)			UNCLASSIFIED	1013
6910	78967655 (22855, 22856)			UNCLASSIFIED	1008, 1019, 1023, 1039
6911	8347474 (22859, 22860)			UNCLASSIFIED	1024
6912	65863670 (22861, 22862)			UNCLASSIFIED	1004
6913	79970189 (22875, 22876)			UNCLASSIFIED	1022
6914	13085245 (22877, 22878)			UNCLASSIFIED	1027
6915	80499553 (22881, 22882)			UNCLASSIFIED	1004, 1006, 1010, 1012, 1017, 1027, 1031
6916	86473996 (22883, 22884)			UNCLASSIFIED	1054
6917	79569041 (22887, 22888)			UNCLASSIFIED	1008
6918	79843760 (22899, 22900)			UNCLASSIFIED	1017
6919	79263014 (22911, 22912)			UNCLASSIFIED	1039

6920	18479772 (22921, 22922)			UNCLASSIFIED	1003
6921	79840476 (22927, 22928)			UNCLASSIFIED	1003, 1008, 1017
6922	80051121 (22929, 22930)			UNCLASSIFIED	1004
6923	20289341 (22933, 22934)			UNCLASSIFIED	1022
6924	80086450 (22939, 22940)			UNCLASSIFIED	1010, 1019, 1041
6925	66368280 (22947, 22948)			UNCLASSIFIED	1004, 1023
6926	95012385 (22949, 22950)			UNCLASSIFIED	1010, 1025
6927	80188104 (22953, 22954)			UNCLASSIFIED	1054, 1058
6928	27844188 (22971, 22972)			UNCLASSIFIED	1024
6929	Novel Protein sim. GBank gi 5031995 ref NP_005663.1 pPSCA - prostate stem cell antigen		Contains protein domain (PF00021) - u-PAR/Ly-6 domain	UNCLASSIFIED	1022, 1024
6930	78793642 (21329, 21330)		Contains protein domain (PF00021) - u-PAR/Ly-6 domain	UNCLASSIFIED	1026, 1038
6931	Novel Protein sim. GBank gi 2589190 (AF005081) - skin-specific protein [Homo sapiens]		Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	1036
6932	Novel Protein sim. GBank gi 5689485 dbj BAA83026.1 - (AB028997) KIAA1074 protein [Homo sapiens]		Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	1026
6933	Novel Protein sim. GBank gi 2495617 sp Q57252 YDIJ_HAEIN - HYPOTHETICAL PROTEIN HI1163		Contains protein domain (PF00037) - 4Fe-4S ferredoxins and related iron- sulfur cluster binding domains.	UNCLASSIFIED	1001, 1004, 1006, 1017, 1022, 1024, 1039

6934	49515922 (147, 148)			Contains protein domain (PF00039) - Fibronectin type I domain	UNCLASSIFIED	1036
6935	78138074 (22695, 22696)			Contains protein domain (PF00039) - Fibronectin type I domain	UNCLASSIFIED	1000, 1001, 1034
6936	78890263 (20293, 20294)			Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	1024
6937	80584323 (7635, 7636)	Novel Protein sim. GBank gij4240225[dbj BAA74891.1] - (AB020675) KIAA0868 protein [Homo sapiens]		Contains protein domain (PF00054) - Laminin G domain	UNCLASSIFIED	1024, 1034, 1036, 1042, 1058
6938	80237102 (7687, 7688)	Novel Protein sim. GBank gij4406188[gib AAD19896] - (AF097637) group IB pancreatic-type secreted phospholipase A2 precursor [Mus musculus]		Contains protein domain (PF00068) - Phospholipase A2	UNCLASSIFIED	1006
6939	78743363 (6051, 6052)	Novel Protein sim. GBank gij134681[sp P00447 SODM_YEAST - SUPEROXIDE DISMUTASE PRECURSOR (MN)		Contains protein domain (PF00081) - Iron/manganese superoxide dismutases (SODM)	UNCLASSIFIED	1022, 1039, 1044
6940	79834189 (2351, 2352)			Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	1000, 1008, 1048
6941	16836028 (11589, 11590)	Novel Protein sim. GBank gij1321818[emb CAA64725] - (X95455) RING zinc finger protein [Gallus gallus]		Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	1003
6942	80503444 (21407, 21408)	Novel Protein sim. GBank gij137670[sp P06422 VE2, HPV08 - REGULATORY PROTEIN E2		Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	1012
6943	25143385 (4317, 4318)			Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	1008
6944	17087159 (20379, 20380)	Novel Protein sim. GBank gij1169927[sp P43794 GLNA_HAEIN - GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE)		Contains protein domain (PF00120) - Glutamine synthetase	UNCLASSIFIED	1023

6945	87459670 (2973, 2974)	Novel Protein sim. GBank gil121356 sp P22248 GLNA_AZOVI - GLUTAMINE SYNTHETASE (GLUTAMATE-- AMMONIA LIGASE)	Contains protein domain (PF00120) - Glutamine synthetase	UNCLASSIFIED	1013, 1015
6946	78763247 (19409, 19410)	Novel Protein sim. GBank gil728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	Contains protein domain (PF00129) - Class I Histocompatibility antigen, domains alpha 1 and 2	UNCLASSIFIED	1017
6947	78745771 (19631, 19632)	Novel Protein sim. GBank gil4836515 gb AAD30477.1 AF12478 - (AF124788) WS-3 protein [Mus musculus]	Contains protein domain (PF00132) - Bacterial transferase hexapeptide (four repeats)	UNCLASSIFIED	1009
6948	90936873 (407, 408)	Novel Protein sim. GBank gil2853081 emb CAA16931.1 - (AL021768) ATP binding protein-like [Arabidopsis thaliana]	Contains protein domain (PF00142) - 4Fe-4S iron sulfur cluster binding proteins, NifH/frxC family	UNCLASSIFIED	1020
6949	32153253 (3463, 3464)	Novel Protein sim. GBank gil113728 sp P24735 AMPC_PSEAE - BETA- LACTAMASE PRECURSOR (CEPHALOSPORINASE)	Contains protein domain (PF00144) - Beta-lactamase	UNCLASSIFIED	1039
6950	19882617 (21827, 21828)	Novel Protein sim. GBank gil1077385 pir J551351 - hypothetical protein YLR348c - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	1022
6951	38327278 (15715, 15716)		Contains protein domain (PF00167) - Fibroblast growth factor	UNCLASSIFIED	1034
6952	37804444 (21709, 21710)	Novel Protein sim. GBank gil2493435 sp Q62261 SPCO_MOUSE - SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1)	Contains protein domain (PF00169) - PH domain	UNCLASSIFIED	1058
6953	86380077 (12399, 12400)	Novel Protein sim. GBank gil2665888 (AF035948) - insulin receptor substrate-3 [Mus musculus]	Contains protein domain (PF00169) - PH domain	UNCLASSIFIED	1053

6954	80056058 (11829, 11830)	Novel Protein sim. GBank gil731674 sp P38713 YHN3_YEAST - HYPOTHETICAL 113.8 KD PROTEIN IN ERG7- NMD2 INTERGENIC REGION	Contains protein domain (PF00169) - PH domain	UNCLASSIFIED	1004
6955	80052396 (20989, 20990)		Contains protein domain (PF00169) - PH domain	UNCLASSIFIED	1004
6956	86673218 (3991, 3992)		Contains protein domain (PF00176) - SNF2 and others N-terminal domain	UNCLASSIFIED	1007
6957	54858942 (22499, 22500)		Contains protein domain (PF00200) - Disintegrin	UNCLASSIFIED	1019
6958	27827840 (16963, 16964)	Novel Protein sim. GBank gil940425 dbj BAA07263 - (D38069) UDP Glucuronosyltransferase [Rattus norvegicus]	Contains protein domain (PF00201) - UDP- glucuronosyl and UDP- glucosyl transferases	UNCLASSIFIED	1022, 1024
6959	36998890 (17263, 17264)	Novel Protein sim. GBank gil1147822 (U10895) - PcaK [Pseudomonas putida]	Contains protein domain (PF00206) - Lyase	UNCLASSIFIED	1001
6960	80412139 (883, 884)	Novel Protein sim. GBank gil120602 sp P07343 FUMH_BACSU - FUMARATE HYDRATASE, CLASS-II (FUMARASE)	Contains protein domain (PF00206) - Lyase	UNCLASSIFIED	1010, 1029
6961	25244080 (9255, 9256)	Novel Protein sim. GBank gil118358 sp P25971 DCOP_BACSU - OROTIDINE 5'-PHOSPHATE DECARBOXYLASE (OMP DECARBOXYLASE)	Contains protein domain (PF00215) - Orotidine 5'- phosphate decarboxylases	UNCLASSIFIED	1008
6962	8754335 (3609, 3610)		Contains protein domain (PF00220) - Neurohypophysial hormones, N-terminal Domain	UNCLASSIFIED	1004
6963	14997971 (9197, 9198)		Contains protein domain (PF00220) - Neurohypophysial hormones, N-terminal Domain	UNCLASSIFIED	1024

6964	79604083 (21899, 21900)	Novel Protein sim. GBank gij2736271 (AF028594) - Trn5501 resolvase [Pseudomonas pseudoalcaligenes]	Contains protein domain (PF00239) - Site-specific recombinases	UNCLASSIFIED	1004
6965	11696111 (19548, 19550)	Novel Protein sim. GBank gij96897 [pir]E42463 - DNA-invertase - Shigella boydii	Contains protein domain (PF00239) - Site-specific recombinases	UNCLASSIFIED	1012, 1034
6966	79172688 (6743, 6744)	Novel Protein sim. GBank gij4503005 [ref]NP_001863.1 pCPB2 - plasma carboxypeptidase B2 precursor	Contains protein domain (PF00246) - Zinc carboxypeptidase	UNCLASSIFIED	1024
6967	78459354 (11657, 11658)	Novel Protein sim. GBank gij731716 [sp]P38836 [YHT2_YEAST - HYPOTHETICAL 49.8 KD PROTEIN IN ACT3-YCK1 INTERGENIC REGION PRECURSOR	Contains protein domain (PF00246) - Zinc carboxypeptidase	UNCLASSIFIED	1026
6968	78897244 (21947, 21948)	Novel Protein sim. GBank gij113580 [sp]P02770 [ALBU_RAT - SERUM ALBUMIN PRECURSOR	Contains protein domain (PF00273) - Serum albumin family	UNCLASSIFIED	1044
6969	56329560 (17671, 17672)	Novel Protein sim. GBank gij203927 (M12450) - vitamin D binding protein prepeptide [Rattus norvegicus]	Contains protein domain (PF00273) - Serum albumin family	UNCLASSIFIED	1017
6970	95287765 (8673, 8674)	Novel Protein sim. GBank gij1706317 [sp]P31848 [DCDA_MYCTU - DIAMINOPIMELATE DECARBOXYLASE (DAP DECARBOXYLASE)	Contains protein domain (PF00278) - Pyridoxal-dependent decarboxylase	UNCLASSIFIED	1008, 1012, 1034, 1038
6971	95005148 (1205, 1206)	Novel Protein sim. GBank gij2494176 [sp]Q04792 [DCEH_YEAST - PUTATIVE GLUTAMATE DECARBOXYLASE (GAD)	Contains protein domain (PF00282) - Pyridoxal-dependent decarboxylase conserved domain	UNCLASSIFIED	1003, 1034
6972	79173016 (1359, 1360)		Contains protein domain (PF00288) - GHMP kinases putative ATP-binding proteins	UNCLASSIFIED	1031
6973	13084179 (12333, 12334)		Contains protein domain (PF00295) - Polygalacturonase (pectinase)	UNCLASSIFIED	1027

6974	80221507 (10413, 10414)	Novel Protein sim. GBank gi 1346913 sp P04046 PUR1_YEAST - AMIDOPHOSPHORIBOSYLTRANSFERASE (GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE) (ATASE)	Contains protein domain (PF00310) - Glutamine amidotransferases class-II	UNCLASSIFIED	1004, 1006, 1008, 1009, 1017, 1022, 1044
6975	94134989 (14357, 14358)	Novel Protein sim. GBank gi 2494417 sp Q43139 F16Q_SACHY - FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC (D-FRUCTOSE-1,6- BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)	Contains protein domain (PF00316) - Fructose-1-6- bisphosphatase	UNCLASSIFIED	1003
6976	86674599 (21475, 21476)	Novel Protein sim. GBank gi 1351856 sp P49608 ACOC_CUCIMA - ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE) (ACONITASE)	Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	UNCLASSIFIED	1007
6977	19883982 (10067, 10068)	Novel Protein sim. GBank gi 4587326 dbj BAA76717.1 - (AB025424) aconitase [Corynebacterium glutamicum]	Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	UNCLASSIFIED	1001
6978	17940404 (12317, 12318)	Novel Protein sim. GBank gi 78222 pir J40996 - phenylalanine 4-monooxygenase (EC 1.14.16.1) - Chromobacterium violaceum	Contains protein domain (PF00351) - Bioplerin- dependent aromatic amino acid hydroxylase	UNCLASSIFIED	1039
6979	11616448 (1907, 1908)	Novel Protein sim. GBank gi 1170299 sp P41809 HKR1_YEAST - HANSENULA MRAKII KILLER TOXIN- RESISTANT PROTEIN 1 PRECURSOR	Contains protein domain (PF00357) - Integrin alpha cytoplasmic region	UNCLASSIFIED	1024
6980	10359028 (15377, 15378)	Novel Protein sim. GBank gi 2947085 (U90263) - organomercurial resistance regulatory protein [Pseudomonas stutzeri]	Contains protein domain (PF00376) - Bacterial regulatory proteins, merR family	UNCLASSIFIED	1039
6981	78527030 (15583, 15584)	Novel Protein sim. GBank gi 2342568 emb CAA74943 - (Y14603) sorbitol phosphotransferase enzyme II [Erwinia amylovora]	Contains protein domain (PF00381) - PTS HPr component phosphorylation sites	UNCLASSIFIED	1008, 1026

6982	10328108 (6315, 6316)			Contains protein domain (PF00391) - PEP-utilizing enzymes	UNCLASSIFIED	1038
6983	32552724 (5573, 5574)	Novel Protein sim. GBank gi 4007683 emb CAA22369 - (AL034443) putative transcriptional regulator [Streptomyces coelicolor]		Contains protein domain (PF00392) - Bacterial regulatory proteins, gntR family	UNCLASSIFIED	1006
6984	78898721 (6165, 6166)	Novel Protein sim. GBank gi 2131430 pir S59790 - hypothetical protein YDR324c - yeast (Saccharomyces cerevisiae)		Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	1017, 1039
6985	29246068 (9547, 9548)	Novel Protein sim. GBank gi 2707295 (AF036931) - root allergen protein [Taraxacum officinale]		Contains protein domain (PF00407) - Pathogenesis-related protein Bet v 1 family	UNCLASSIFIED	1026
6986	78365892 (1845, 1846)	Novel Protein sim. GBank gi 2131456 pir S61174 - hypothetical protein YDR379w - yeast (Saccharomyces cerevisiae)		Contains protein domain (PF00412) - LIM domain containing proteins	UNCLASSIFIED	1003
6987	79859913 (427, 428)	Novel Protein sim. GBank gi 2983549 (AE000721) - transcriptional regulator (TetR/AcrR family) [Aquifex aeolicus]		Contains protein domain (PF00440) - Bacterial regulatory proteins, tetR family	UNCLASSIFIED	1044
6988	66154240 (12229, 12230)	Novel Protein sim. GBank gi 2343271 (AF014793) - pol polyprotein [walleye epidermal hyperplasia virus type 2]		Contains protein domain (PF00446) - Gonadotropin-releasing hormones	UNCLASSIFIED	1024
6989	21414443 (6979, 6980)			Contains protein domain (PF00446) - Gonadotropin-releasing hormones	UNCLASSIFIED	1022
6990	91254670 (22049, 22050)	Novel Protein sim. GBank gi 226039 prf 1408163B - CPase II B [Hordeum vulgare var. distichum]		Contains protein domain (PF00450) - Serine carboxypeptidase	UNCLASSIFIED	1010
6991	80063181 (5957, 5958)	Novel Protein sim. GBank gi 2460272 (AF020809) - transcriptional activator DeoR [Salmonella typhimurium]		Contains protein domain (PF00455) - Bacterial regulatory proteins, deoR family	UNCLASSIFIED	1003, 1010

6992	54996162 (21795, 21796)	Novel Protein sim. GBank gil1358093[dbj BAA31996] - (AB015975) Glp repressor [Pseudomonas tolaasii]	Contains protein domain (PF00455) - Bacterial regulatory proteins, deoR family	UNCLASSIFIED	1029
6993	2028342 (5899, 5900)	Novel Protein sim. GBank gil1175508[sp P45388]YAEJ_PSEPU - HYPOTHETICAL 15.2 KD PROTEIN IN PCAJ 3'REGION	Contains protein domain (PF00472) - Prokaryotic-type class I peptide chain release factors	UNCLASSIFIED	1034
6994	27980856 (22923, 22924)	Novel Protein sim. GBank gil1175508[sp P45388]YAEJ_PSEPU - HYPOTHETICAL 15.2 KD PROTEIN IN PCAJ 3'REGION	Contains protein domain (PF00472) - Prokaryotic-type class I peptide chain release factors	UNCLASSIFIED	1006
6995	21425931 (7211, 7212)	Novel Protein sim. GBank gil1350576[sp P47849]RF1_COXBU - PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1).	Contains protein domain (PF00472) - Prokaryotic-type class I peptide chain release factors	UNCLASSIFIED	1022
6996	79582998 (17459, 17460)	Novel Protein sim. GBank gil1175188[sp P44572]Y213_HAEIN - PUTATIVE BINDING PROTEIN H10213 PRECURSOR	Contains protein domain (PF00496) - Bacterial extracellular solute-binding proteins, family 5	UNCLASSIFIED	1022, 1031
6997	39507876 (5303, 5304)	Novel Protein sim. GBank gil2131533[pirj S69559] - hypothetical protein YDR501w - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00498) - Forkhead-associated (FHA) domain	UNCLASSIFIED	1024
6998	65642469 (15455, 15456)		Contains protein domain (PF00511) - E2 (early) protein, C terminal	UNCLASSIFIED	1016
6999	85519544 (13709, 13710)	Novel Protein sim. GBank gil134515[sp P17883]SKI3_YEAST - SUPERKILLER 3 PROTEIN	Contains protein domain (PF00515) - TPR Domain	UNCLASSIFIED	1001, 1003, 1006, 1008, 1009, 1010, 1012, 1016, 1017, 1022, 1023, 1024, 1025, 1026, 1027, 1034, 1038, 1039, 1044, 1049

7000	25256567 (20099, 20100)	Novel Protein sim. GBank gjl3859116 (AF031609) - unknown [<i>Oryza sativa</i>]	Contains protein domain (PF00515) - TPR Domain	UNCLASSIFIED	1003
7001	78735744 (16201, 16202)		Contains protein domain (PF00518) - Early Protein (E6)	UNCLASSIFIED	1009
7002	80074461 (17023, 17024)	Novel Protein sim. GBank gjl2131472 pir S69691 - hypothetical protein YDR409w - yeast (<i>Saccharomyces cerevisiae</i>)	Contains protein domain (PF00526) - Dictyostelium (slime mold) repeats	UNCLASSIFIED	1008, 1009, 1017, 1022, 1026, 1031
7003	80216295 (21511, 21512)	Novel Protein sim. GBank gjl584850 sp P38041 BOB1_YEAST - BOB1 PROTEIN (BEM1-BINDING PROTEIN)	Contains protein domain (PF00536) - SAM domain (Sterile alpha motif)	UNCLASSIFIED	1003, 1004, 1006, 1008, 1012, 1017, 1022, 1024, 1025, 1034, 1044
7004	78918982 (12745, 12746)	Novel Protein sim. GBank gjl1711572 sp P53586 SUCA_ARATH - SUCCINYL-COA LIGASE (GDP-FORMING), ALPHA-CHAIN PRECURSOR (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN) (SCS-ALPHA)	Contains protein domain (PF00549) - CoA-ligases	UNCLASSIFIED	1039
7005	20287765 (14469, 14470)	Novel Protein sim. GBank gjl4512118 gb AAD21623.1 - (AF128399) succinyl-CoA synthetase alpha subunit [<i>Pseudomonas aeruginosa</i>]	Contains protein domain (PF00549) - CoA-ligases	UNCLASSIFIED	1034
7006	17889249 (3319, 3320)		Contains protein domain (PF00553) - Cellulose binding domain	UNCLASSIFIED	1044
7007	25333573 (11123, 11124)	Novel Protein sim. GBank gjl3024880 sp O05832 Y1DE_MYCTU - HYPOTHETICAL 47.2 KD PROTEIN CY27.14	Contains protein domain (PF00571) - CBS domain	UNCLASSIFIED	1008
7008	80431234 (16731, 16732)	Novel Protein sim. GBank gjl3261746 emb CAB08449 - (Z95207) nusA [<i>Mycobacterium tuberculosis</i>]	Contains protein domain (PF00575) - S1 RNA binding domain	UNCLASSIFIED	1004, 1006, 1010, 1012, 1022, 1023, 1024, 1031, 1034, 1038

7009	79953893 (22287, 22288)			Contains protein domain (PF00583) - Acetyltransferase (GNAT) family	UNCLASSIFIED	1017, 1026, 1039
7010	80497391 (17979, 17980)	Novel Protein sim. GBank gij2909501[embjCAA17386] - (AL021931) hypothetical protein Rv0380c [Mycobacterium tuberculosis]		Contains protein domain (PF00588) - SpoU rRNA Methylase family	UNCLASSIFIED	1003, 1004, 1010, 1012, 1024, 1027, 1034
7011	19521786 (15213, 15214)	Novel Protein sim. GBank gij586908[spjQ06753]YACO_BACSU - HYPOTHETICAL TRNA ^{RRNA} METHYLTRANSFERASE YACO		Contains protein domain (PF00588) - SpoU rRNA Methylase family	UNCLASSIFIED	1034
7012	79859334 (2751, 2752)	Novel Protein sim. GBank gij1552728 (U70214) - ferrichrome-iron receptor precursor [Escherichia coli]		Contains protein domain (PF00593) - TonB dependent receptor C-terminal region	UNCLASSIFIED	1017
7013	10870503 (5791, 5792)	Novel Protein sim. GBank gij95824[pirj]S09262 - ferric-coprogen receptor protein precursor - Escherichia coli		Contains protein domain (PF00593) - TonB dependent receptor C-terminal region	UNCLASSIFIED	1031
7014	79831934 (2055, 2056)	Novel Protein sim. GBank gij116515[spjP22137]CLH_YEAST - CLATHRIN HEAVY CHAIN		Contains protein domain (PF00637) - 7-fold repeat in Clathrin and VPS	UNCLASSIFIED	1006, 1008
7015	79759680 (16601, 16602)	Novel Protein sim. GBank gij731822[spjP40516]YIG4_YEAST - HYPOTHETICAL 28.7 KD PROTEIN IN RNR3-ARC15 INTERGENIC REGION		Contains protein domain (PF00638) - RanBP1 domain.	UNCLASSIFIED	1023
7016	80236362 (1293, 1294)	Novel Protein sim. GBank gij1166450[embjCAA64559] - (X95262) Tfm5 [Lycopodium obscurum]		Contains protein domain (PF00642) - Zinc finger C-x8-C-x5-C-x3-H type (and similar).	UNCLASSIFIED	1033, 1034
7017	9286521 (19447, 19448)	Novel Protein sim. GBank gij538258 (L01880) - elongation factor 1-gamma [Saccharomyces cerevisiae]		Contains protein domain (PF00647) - Elongation factor 1 gamma, conserved domain.	UNCLASSIFIED	1008

7018	11394894 (6027, 6028)	Novel Protein sim. GBank gij1077336 pir S51467 hypothetical protein YLR380w - Yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00650) - CRAL/TRIO domain.	UNCLASSIFIED	1010
7019	80237349 (18083, 18084)	Novel Protein sim. GBank gij395288 emb CAA52227 - (X74130) URF (Saccharomyces cerevisiae)	Contains protein domain (PF00650) - CRAL/TRIO domain.	UNCLASSIFIED	1010, 1017, 1022, 1034
7020	80496847 (12421, 12422)	Novel Protein sim. GBank gij2267235 (U69874) - delayed anaerobic 1 (Saccharomyces cerevisiae)	Contains protein domain (PF00650) - Seripauperin and TIP1 family.	UNCLASSIFIED	1001, 1003, 1008, 1009, 1010, 1012, 1017, 1022, 1023, 1026, 1027, 1034, 1038, 1039, 1054
7021	80500790 (21009, 21010)	Novel Protein sim. GBank gij418400 sp P32612 PAU2_YEAST - PAU2 PROTEIN	Contains protein domain (PF00650) - Seripauperin and TIP1 family.	UNCLASSIFIED	1004, 1006, 1010, 1012, 1022, 1023, 1024, 1025, 1029, 1031, 1034, 1038
7022	14401607 (13865, 13866)	Novel Protein sim. GBank gij2506427 sp Q03843 FLAA_HELPY - FLAGELLIN A	Contains protein domain (PF00669) - Bacterial flagellin N-terminus	UNCLASSIFIED	1053
7023	8230925 (10797, 10798)	Novel Protein sim. GBank gij731306 sp P39548 YAJ8_YEAST - HYPOTHETICAL 26.5 KD PROTEIN IN CDC15-YAT1 INTERGENIC REGION	Contains protein domain (PF00674) - DUP family of yeast membrane proteins	UNCLASSIFIED	1022
7024	79423061 (1281, 1282)	Novel Protein sim. GBank gij3978254 gb AAC83237.1 - (AF072374) beta-N-acetylglucosaminidase [Pseudoalteromonas sp. S9]	Contains protein domain (PF00728) - Glycosyl hydrolase family 20	UNCLASSIFIED	1017
7025	79462065 (3727, 3728)		Contains protein domain (PF00796) - Photosystem I reaction centre subunit VIII	UNCLASSIFIED	1034

7026	78895515 (10145, 10146)	Novel Protein sim. GBank glj3980413 (AC004561) - pumilio-like protein [Arabidopsis thaliana]	Contains protein domain (PF00806) - Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)	UNCLASSIFIED	1023
7027	49222609 (15557, 15558)		Contains protein domain (PF00807) - Apidaecin	UNCLASSIFIED	1040
7028	80504167 (8393, 8394)	Novel Protein sim. GBank glj549104 sp P35880 TRA1_LACHE - TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS1201	Contains protein domain (PF00872) - Transposase, Mutator family	UNCLASSIFIED	1012
7029	66258458 (755, 756)	Novel Protein sim. GBank glj549105 sp P35882 TRA1_MYCTU - TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS1081	Contains protein domain (PF00872) - Transposase, Mutator family	UNCLASSIFIED	1010
7030	6427565 (18101, 18102)	Novel Protein sim. GBank glj549115 sp P35879 TRA_CORDI - PROBABLE TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT	Contains protein domain (PF00872) - Transposase, Mutator family	UNCLASSIFIED	1058
7031	78937340 (22893, 22894)	Novel Protein sim. GBank glj2983282 (AE000702) - cation efflux system (AcrB/AcrD/AcrF family) [Aquifex aeolicus]	Contains protein domain (PF00873) - AcrB/AcrD/AcrF family	UNCLASSIFIED	1039
7032	65707976 (10013, 10014)		Contains protein domain (PF00873) - AcrB/AcrD/AcrF family	UNCLASSIFIED	1023
7033	87453741 (21577, 21578)	Novel Protein sim. GBank glj3687389 emb CAA76074 - (Y16124) putative cullin protein [Lycopersicon esculentum]	Contains protein domain (PF00888) - Cullin family	UNCLASSIFIED	1025
7034	27804713 (11325, 11326)	Novel Protein sim. GBank glj4503161 ref NP_003583.1 pCUL1 - cullin 1	Contains protein domain (PF00888) - Cullin family	UNCLASSIFIED	1024, 1034, 1039
7035	80233839 (1951, 1952)	Novel Protein sim. GBank glj5139634 emb CAB45563.1 - (AL079353) putative penicillin-binding protein [Streptomyces coelicolor]	Contains protein domain (PF00912) - Transglycosylase	UNCLASSIFIED	1006, 1008, 1010, 1017, 1026, 1038, 1039

7036	79906077 (20757, 20758)	Novel Protein sim. GBank gij2995295[emb]CAA18324] - (AL022268) hypothetical protein SC4H2.08 [Streptomyces coelicolor]	Contains protein domain (PF00919) - Uncharacterized protein family UPF0004	UNCLASSIFIED	1012, 1023
7037	95292844 (5631, 5632)	Novel Protein sim. GBank gij3294240[emb]CAA19853] - (AL031031) hypothetical protein SC7C7.07 [Streptomyces coelicolor]	Contains protein domain (PF00919) - Uncharacterized protein family UPF0004	UNCLASSIFIED	1006, 1010, 1024
7038	78942693 (16873, 16874)		Contains protein domain (PF01006) - Hepatitis C virus non-structural protein NS4a	UNCLASSIFIED	1038
7039	37803971 (5097, 5098)	Novel Protein sim. GBank gij631857[pir]A41558 - N-syndecan - rat (fragment)	Contains protein domain (PF01034) - Syndecan domain	UNCLASSIFIED	1058
7040	78678192 (17715, 17716)	Novel Protein sim. GBank gij1074872[pir]C64173 - hypothetical protein H11627 - Haemophilus influenzae (strain Rd KW20)	Contains protein domain (PF01042) - Domain of unknown function	UNCLASSIFIED	1008, 1017
7041	19879670 (13791, 13792)	Novel Protein sim. GBank gij3820514 (AF061751) - LysR-type transcriptional regulator PhnS [Burkholderia sp. RP007]	Contains protein domain (PF01046) - NodD transcription activator carboxyl terminal region	UNCLASSIFIED	1034
7042	47656797 (11407, 11408)	Novel Protein sim. GBank gij586346[sp]P38138[YB79_YEAST - PUTATIVE FAMILY 31 GLUCOSIDASE IN PCS60-ABD1 INTERGENIC REGION	Contains protein domain (PF01055) - Glycosyl hydrolases family 31	UNCLASSIFIED	1029
7043	79162929 (18741, 18742)	Novel Protein sim. GBank gij5420387[emb]CAB48679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF01106) - Nifu-like domain	UNCLASSIFIED	1004, 1026, 1044
7044	17900428 (17557, 17558)	Novel Protein sim. GBank gij1169716[sp]P44788[SUN_HAEIN - SUN PROTEIN (FMU PROTEIN)]	Contains protein domain (PF01189) - NOL1/NOP2/sun family	UNCLASSIFIED	1031, 1044

7045	79600399 (2459, 2460)	Novel Protein sim. GBank gi 128399 sp P14743 NMNT_YEAST - GLYCYLPEPTIDE N- TETRADECANOYLTRANSFERASE (PEPTIDE N- MYRISTOYLTRANSFERASE) (MYRISTOYL- COA:PROTEIN N-MYRISTOYLTRANSFERASE) (NMNT)	Contains protein domain (PF01233) - Myristoyl- CoA:protein N- myristoyltransferase	UNCLASSIFIED	1024, 1025
7046	87453362 (16123, 16124)	Novel Protein sim. GBank gi 462195 sp P33278 SUI1_ORYSA - PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)	Contains protein domain (PF01253) - Translation initiation factor SUI1	UNCLASSIFIED	1022, 1025
7047	78985624 (6401, 6402)	Novel Protein sim. GBank gi 230281 pdb 1R69 - 434 Repressor (Amino-Terminal Domain) (R1-69)	Contains protein domain (PF01381) - Helix-turn-helix	UNCLASSIFIED	1016, 1022
7048	13883824 (13601, 13602)	Novel Protein sim. GBank gi 4154729 (AE001459) - putative [Helicobacter pylori J99]	Contains protein domain (PF01402) - Helix-turn-helix protein, copG family	UNCLASSIFIED	1053
7049	80245946 (7697, 7698)	Novel Protein sim. GBank gi 172947 (J03965) - Phe-RNA synthetase [Saccharomyces cerevisiae]	Contains protein domain (PF01409) - tRNA synthetases class II (F)	UNCLASSIFIED	1003, 1006, 1008, 1022, 1034, 1044
7050	79167929 (21197, 21198)	Novel Protein sim. GBank gi 3880625 emb CAB07858 - (Z93785) predicted using GeneFinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST EMBL: T01682 comes from this gene; cDNA EST EMBL: M75823 comes from this gene; cDNA EST EMBL: D27559 comes from this ge...	Contains protein domain (PF01412) - Putative GTP- ase activating protein for Arf	UNCLASSIFIED	1031, 1050
7051	78471143 (7969, 7970)	Novel Protein sim. GBank gi 4582434 gb AAD24820.1 AC00719 - (AC007196) unknown protein [Arabidopsis thaliana]	Contains protein domain (PF01423) - Sm protein	UNCLASSIFIED	1053
7052	46893429 (14041, 14042)	Novel Protein sim. GBank gi 320483 pir J060634 - probable transposase IS257/3 - Staphylococcus aureus plasmid pSH6	Contains protein domain (PF01438) - Transposase	UNCLASSIFIED	1034

7053	65466599 (1925, 1926)	Novel Protein sim. GBank gi 4753138 gb AAD28804.1 - (U52844) KdtB [Serratia marcescens]	Contains protein domain (PF01467) - Cytidylyltransferase	UNCLASSIFIED	1010
7054	80045310 (5257, 5258)	Novel Protein sim. GBank gi 5689884 emb CAB52047.1 - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)]	Contains protein domain (PF01479) - S4 domain	UNCLASSIFIED	1006, 1024, 1034, 1038, 1054
7055	54820637 (18225, 18226)	Novel Protein sim. GBank gi 481462 pir S38653 - transposase - Klebsiella pneumoniae	Contains protein domain (PF01526) - Transposase	UNCLASSIFIED	1029
7056	79258045 (1259, 1260)	Novel Protein sim. GBank gi 2132817 pir S61981 - probable membrane protein YOL003c - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF01529) - DHHC zinc finger domain	UNCLASSIFIED	1003, 1008, 1009
7057	13521641 (16399, 16400)		Contains protein domain (PF01581) - FMRFamide related peptide family	UNCLASSIFIED	1024
7058	20293179 (17, 18)	Novel Protein sim. GBank gi 3122208 sp Q49776 HIS1_MYCLE - ATP PHOSPHORIBOSYLTRANSFERASE	Contains protein domain (PF01634) - ATP phosphoribosyltransferase	UNCLASSIFIED	1034
7059	79815141 (10003, 10004)	Novel Protein sim. GBank gi 2076670 emb CAB08387 - (Z95150) hypothetical protein Rv3095 [Mycobacterium tuberculosis]	Contains protein domain (PF01638) - Protein of unknown function	UNCLASSIFIED	1044
7060	13085662 (6503, 6504)	Novel Protein sim. GBank gi 140807 sp P24536 Y121_BURCE - INSERTION ELEMENT IS402 HYPOTHETICAL 24 KD PROTEIN	Contains protein domain (PF01675) - Transposase	UNCLASSIFIED	1027
7061	80306881 (22435, 22436)	Novel Protein sim. GBank gi 1175962 sp P43545 SNZ3_YEAST - SNZ3 PROTEIN	Contains protein domain (PF01680) - Uncharacterized protein family SNZ	UNCLASSIFIED	1001, 1003, 1006, 1008, 1009, 1012, 1017, 1022, 1023, 1024, 1026, 1029, 1031, 1034, 1044, 1053

7062	13901544 (22701, 22702)	Novel Protein sim. GBank gil2501577 sp Q03148 SNZ1_YEAST - SNZ1 PROTEIN (P35)	Contains protein domain (PF01680) - Uncharacterized protein family SNZ	UNCLASSIFIED	1053
7063	95293073 (1365, 1366)	Novel Protein sim. GBank gil140888 sp P27847 YIGK_ECOLI - HYPOTHETICAL 15.4 KD PROTEIN IN RECQ- PLDB INTERGENIC REGION (F138)	Contains protein domain (PF01810) - LysE type translocator	UNCLASSIFIED	1024
7064	78695814 (237, 238)	Novel Protein sim. GBank gil1001388 dbj BAA10878 - (D64006) hypothetical protein [Synecocystis sp.]		UNCLASSIFIED	1003
7065	9842251 (4811, 4812)	Novel Protein sim. GBank gil1001430 dbj BAA10054 - (D63999) ORF1 [Synecocystis sp.]		UNCLASSIFIED	1039
7066	80081532 (12373, 12374)	Novel Protein sim. GBank gil1001462 dbj BAA10088 - (D63999) hypothetical protein [Synecocystis sp.]		UNCLASSIFIED	1034
7067	16398835 (15325, 15326)	Novel Protein sim. GBank gil1001499 dbj BAA10124 - (D64000) hypothetical protein [Synecocystis sp.]		UNCLASSIFIED	1003
7068	80051064 (2749, 2750)	Novel Protein sim. GBank gil1001663 dbj BAA10397 - (D64002) rare lipoprotein A [Synecocystis sp.]		UNCLASSIFIED	1004, 1010
7069	57301027 (2691, 2692)	Novel Protein sim. GBank gil1001939 (U13152) - guanine nucleotide-binding protein beta 5 [Mesocricetus auratus]		UNCLASSIFIED	1004, 1006, 1010, 1022, 1024, 1034, 1044
7070	79187134 (7223, 7224)	Novel Protein sim. GBank gil1006592 dbj BAA10745 - (D64005) magnesium and cobalt transport protein [Synecocystis sp.]		UNCLASSIFIED	1024
7071	80237636 (12631, 12632)	Novel Protein sim. GBank gil101245 pir S15038 - cell division control protein CDC15 - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1001, 1004, 1006, 1009, 1025, 1026, 1034

7072	78376629 (7515, 7516)	Novel Protein sim. GBank gil102058 pir C41710 - promastigote surface antigen-2 (clone 2.5) - Leishmania major (fragment)		UNCLASSIFIED	1008
7073	80503459 (22669, 22670)	Novel Protein sim. GBank gil102427 pir D41132 - collagen-related protein 4 - Hydra magnipapillata (fragment)		UNCLASSIFIED	1003, 1006, 1008, 1009, 1010, 1012, 1016, 1022, 1023, 1034, 1044, 1049
7074	32309196 (13443, 13444)	Novel Protein sim. GBank gil106040 pir A39530 - fragile X mental retardation syndrome protein FMR1 - human (fragment)		UNCLASSIFIED	1029
7075	30537137 (3567, 3568)	Novel Protein sim. GBank gil106322 pir B34087 - hypothetical protein (L1H 3' region) - human		UNCLASSIFIED	1026
7076	54700862 (4167, 4168)	Novel Protein sim. GBank gil106322 pir B34087 - hypothetical protein (L1H 3' region) - human		UNCLASSIFIED	1036
7077	30530736 (8071, 8072)	Novel Protein sim. GBank gil106322 pir B34087 - hypothetical protein (L1H 3' region) - human		UNCLASSIFIED	1026
7078	55894344 (10621, 10622)	Novel Protein sim. GBank gil106322 pir B34087 - hypothetical protein (L1H 3' region) - human		UNCLASSIFIED	1038
7079	86685724 (21537, 21538)	Novel Protein sim. GBank gil106322 pir B34087 - hypothetical protein (L1H 3' region) - human		UNCLASSIFIED	1029
7080	23286017 (14673, 14674)	Novel Protein sim. GBank gil106323 pir A34087 - hypothetical protein (L1H 5' region) - human		UNCLASSIFIED	1003
7081	77879807 (12881, 12882)	Novel Protein sim. GBank gil106903 pir B28096 - line-1 protein ORF2 - human		UNCLASSIFIED	1019

7082	94137421 (16359, 16360)	Novel Protein sim. GBank gij106903 pir B28096 - line-1 protein ORF2 - human		UNCLASSIFIED	1016, 1044
7083	33205928 (22903, 22904)	Novel Protein sim. GBank gij1072396 emb CAA63735.1 - (X933358) phaB [Sinorhizobium meliloti]		UNCLASSIFIED	1026
7084	20733832 (18513, 18514)	Novel Protein sim. GBank gij1072397 emb CAA63736.1 - (X933358) phaC [Sinorhizobium meliloti]		UNCLASSIFIED	1006
7085	79833309 (17331, 17332)	Novel Protein sim. GBank gij1074127 pir D64108 - gluconate permease (gntP) homolog - Haemophilus influenzae (strain Rd KW20)		UNCLASSIFIED	1023
7086	13083321 (1795, 1796)	Novel Protein sim. GBank gij1074506 pir C64158 - hypothetical protein HI0755 - Haemophilus influenzae (strain Rd KW20)		UNCLASSIFIED	1031
7087	54856328 (11431, 11432)	Novel Protein sim. GBank gij107621 pir S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	1019
7088	29347055 (4003, 4004)	Novel Protein sim. GBank gij1076660 pir S51839 - D13F(MYBST1) protein - potato		UNCLASSIFIED	1022
7089	30631920 (6269, 6270)	Novel Protein sim. GBank gij1076660 pir S51839 - D13F(MYBST1) protein - potato		UNCLASSIFIED	1022
7090	65654694 (12199, 12200)	Novel Protein sim. GBank gij1076802 pir S49915 - extensin-like protein - maize		UNCLASSIFIED	1054
7091	11306338 (19461, 19462)	Novel Protein sim. GBank gij1076996 pir S49755 - adenine phosphoribosyltransferase (EC 2.4.2.7) 1 - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1024
7092	78759044 (8201, 8202)	Novel Protein sim. GBank gij1077123 pir S50383 - gamma-glutamyltransferase homolog YLR299w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1017, 1044

7093	79915055 (10669, 10670)	Novel Protein sim. GBank gi 1077123 pir S50383 - gamma-glutamyltransferase homolog YLR299w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1017
7094	25335671 (14029, 14030)	Novel Protein sim. GBank gi 1077162 pir S52504 - probable membrane protein YDL015c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1039
7095	78787902 (12971, 12972)	Novel Protein sim. GBank gi 1077164 pir S52500 - SWH1 protein homolog YDL019c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1026
7096	94986339 (17901, 17902)	Novel Protein sim. GBank gi 1077164 pir S52500 - SWH1 protein homolog YDL019c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1034
7097	79242609 (2845, 2846)	Novel Protein sim. GBank gi 1077187 pir S49777 - probable membrane protein YDR180w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003, 1017
7098	10167049 (22757, 22758)	Novel Protein sim. GBank gi 1077257 pir S52522 - hypothetical protein YPL009c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1034
7099	78778585 (6573, 6574)	Novel Protein sim. GBank gi 1077258 pir S52524 - probable membrane protein YPL007c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1009
7100	30274057 (18497, 18498)	Novel Protein sim. GBank gi 1077258 pir S52524 - probable membrane protein YPL007c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1026
7101	29354457 (1595, 1596)	Novel Protein sim. GBank gi 1077307 pir S51892 - probable membrane protein YOL105c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003

7102	79316556 (11869, 11870)	Novel Protein sim. GBank gi 1077324 pir S50965 - probable membrane protein YLL055w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1004
7103	79398033 (3937, 3938)	Novel Protein sim. GBank gi 1077335 pir S51468 - probable membrane protein YLR381w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006
7104	80218264 (8285, 8286)	Novel Protein sim. GBank gi 1077350 pir S50381 - probable membrane protein YLR297w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1001, 1009, 1022, 1023, 1039
7105	80503416 (17911, 17912)	Novel Protein sim. GBank gi 1077361 pir S51391 - probable membrane protein YLR373c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003, 1004, 1008, 1009, 1012, 1017, 1023, 1024, 1030, 1038, 1044
7106	3869284 (20811, 20812)	Novel Protein sim. GBank gi 1077361 pir S51391 - probable membrane protein YLR373c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1026
7107	82060755 (10721, 10722)	Novel Protein sim. GBank gi 1077393 pir S51403 - probable membrane protein YLR266c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1008, 1012, 1016, 1022, 1034
7108	10205513 (6135, 6136)	Novel Protein sim. GBank gi 1077401 pir S51413 - probable membrane protein YLR277c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006
7109	65694988 (22593, 22594)	Novel Protein sim. GBank gi 1077404 pir S51422 - probable membrane protein YLR177w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1038
7110	78938649 (12835, 12836)	Novel Protein sim. GBank gi 1077407 pir S51435 - hypothetical protein YLR190w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1022, 1044

7111	82342298 (3041, 3042)	Novel Protein sim. GBank gi 1077412 pir S51432 - hypothetical protein YLR187w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1001
7112	65892183 (14115, 14116)	Novel Protein sim. GBank gi 1077416 pir S51464 - probable membrane protein YLR356w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006, 1016
7113	65482988 (3263, 3264)	Novel Protein sim. GBank gi 1077417 pir S51460 - hypothetical protein YLR352w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1023
7114	39375938 (19281, 19282)	Novel Protein sim. GBank gi 1077551 pir S54034 - probable membrane protein YDR049w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1010
7115	78792449 (17545, 17546)	Novel Protein sim. GBank gi 1077705 pir S50633 - hypothetical protein YER130c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1009
7116	30265873 (633, 634)	Novel Protein sim. GBank gi 1077900 pir S57113 - BUD4 protein - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1026
7117	78758427 (3415, 3416)	Novel Protein sim. GBank gi 1078071 pir S53398 - hypothetical protein YLR320w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1009, 1026, 1044
7118	79861629 (21087, 21088)	Novel Protein sim. GBank gi 1078081 pir S53392 - probable membrane protein YLR313c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1022, 1038
7119	78990389 (12681, 12682)	Novel Protein sim. GBank gi 1078147 pir S54389 - NCA2 protein - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003, 1039
7120	28488943 (9767, 9768)	Novel Protein sim. GBank gi 1078508 pir S54640 - KCS1 protein - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1023
7121	56147697 (21979, 21980)	Novel Protein sim. GBank gi 1082459 pir A55641 - homeotic protein GAX - human		UNCLASSIFIED	1023

7122	27843871 (15223, 15224)	Novel Protein sim. GBank gjl1083428 pir S54876 - NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) precursor - mouse		UNCLASSIFIED	1004, 1009, 1010, 1022, 1034
7123	78378457 (11711, 11712)	Novel Protein sim. GBank gjl1084084 pir S55811 - hrpA protein - Escherichia coli		UNCLASSIFIED	1026
7124	19637731 (1019, 1020)	Novel Protein sim. GBank gjl1084554 pir S52597 - probable membrane protein YHR070c-a - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006
7125	27929546 (5069, 5070)	Novel Protein sim. GBank gjl1084595 pir S53561 - probable membrane protein YAL056c-a - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006
7126	80258617 (13919, 13920)	Novel Protein sim. GBank gjl1084783 pir S54079 - BRR1 protein - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1010, 1022, 1034, 1038
7127	79256123 (5079, 5080)	Novel Protein sim. GBank gjl110587 bbs 170532 - (S79410) nuclear localization signals (NLS)-binding protein=spot-1 [mice, Balb/c, testes, Peptide, 140 aa] [Mus sp.]		UNCLASSIFIED	1003, 1029
7128	80428421 (5623, 5624)	Novel Protein sim. GBank gjl110587 bbs 170532 - (S79410) nuclear localization signals (NLS)-binding protein=spot-1 [mice, Balb/c, testes, Peptide, 140 aa] [Mus sp.]		UNCLASSIFIED	1003, 1010, 1024, 1025, 1053
7129	80061887 (8855, 8856)	Novel Protein sim. GBank gjl110587 bbs 170532 - (S79410) nuclear localization signals (NLS)-binding protein=spot-1 [mice, Balb/c, testes, Peptide, 140 aa] [Mus sp.]		UNCLASSIFIED	1034

7130	29012667 (15548, 15550)	Novel Protein sim. GBank gij1110587 bbs1170532 - (S79410) nuclear localization signals (NLS)-binding protein=spot-1 [mice, Balb/c, testes, Peptide, 140 aa] [Mus sp.]	UNCLASSIFIED	1017
7131	78251974 (16655, 16656)	Novel Protein sim. GBank gij1110587 bbs1170532 - (S79410) nuclear localization signals (NLS)-binding protein=spot-1 [mice, Balb/c, testes, Peptide, 140 aa] [Mus sp.]	UNCLASSIFIED	1026
7132	78461462 (21339, 21340)	Novel Protein sim. GBank gij1110587 bbs1170532 - (S79410) nuclear localization signals (NLS)-binding protein=spot-1 [mice, Balb/c, testes, Peptide, 140 aa] [Mus sp.]	UNCLASSIFIED	1003
7133	98220393 (15237, 15238)	Novel Protein sim. GBank gij1111134 pir1S22934 - testis-specific protein (clone 46) - mouse (fragment)	UNCLASSIFIED	1026, 1031
7134	20608237 (3281, 3282)	Novel Protein sim. GBank gij113450 sp P07248 ADR1_YEAST - REGULATORY PROTEIN ADR1	UNCLASSIFIED	1004, 1022
7135	66489949 (591, 592)	Novel Protein sim. GBank gij113620 sp P11604 ALF_ECOLI - FRUCTOSE-BISPHOSPHATE ALDOLASE CLASS II	UNCLASSIFIED	1029
7136	21436050 (17323, 17324)	Novel Protein sim. GBank gij113670 sp P23963 ALUE_HUMAN - IIII ALU CLASS E WARNING ENTRY IIII	UNCLASSIFIED	1022
7137	8754246 (12355, 12356)	Novel Protein sim. GBank gij113751 sp P15034 AMPP_ECOLI - XAA-PRO AMINOPEPTIDASE (X-PRO AMINOPEPTIDASE) (AMINOPEPTIDASE P II) (APP-II) (AMINOACYLPROLINE AMINOPEPTIDASE)	UNCLASSIFIED	1004
7138	79633247 (19999, 20000)	Novel Protein sim. GBank gij114113 sp P13981 ARCA_PSEAE - ARGININE DEIMINASE	UNCLASSIFIED	1022, 1038

7139	30243994 (3187, 3188)	Novel Protein sim. GBank gil114947 sp P16279 BGAM_HUMAN - BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR		UNCLASSIFIED	1026
7140	8018931 (16557, 16558)	Novel Protein sim. GBank gil115910 sp P16522 CC23_YEAST - CELL DIVISION CONTROL PROTEIN 23		UNCLASSIFIED	1058
7141	27962453 (20491, 20492)	Novel Protein sim. GBank gil115914 sp P04821 CC25_YEAST - CELL DIVISION CONTROL PROTEIN 25		UNCLASSIFIED	1034
7142	25321510 (22815, 22816)	Novel Protein sim. GBank gil115936 sp P06103 IF3X_YEAST - EUKARYOTIC TRANSLATION INITIATION FACTOR 3 BETA SUBUNIT (EIF-3 BETA) (EIF3 P90) (CELL CYCLE REGULATION AND TRANSLATION INITIATION PROTEIN)		UNCLASSIFIED	1022
7143	29345595 (4595, 4596)	Novel Protein sim. GBank gil116515 sp P22137 CLH_YEAST - CLATHRIN HEAVY CHAIN		UNCLASSIFIED	1006, 1012, 1022, 1031, 1054
7144	80060929 (3471, 3472)	Novel Protein sim. GBank gil1168262 sp P44425 AAT_HAEIN - ASPARTATE AMINOTRANSFERASE (TRANSAMINASE A) (ASPAT)		UNCLASSIFIED	1008, 1017, 1024, 1044
7145	10209161 (12847, 12848)	Novel Protein sim. GBank gil1168816 sp P30665 CC54_YEAST - CELL DIVISION CONTROL PROTEIN 54		UNCLASSIFIED	1025
7146	80224008 (6259, 6260)	Novel Protein sim. GBank gil1169151 sp P08678 CYAA_YEAST - ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE)		UNCLASSIFIED	1006, 1023, 1024, 1027
7147	17963110 (16817, 16818)	Novel Protein sim. GBank gil1169152 sp P40127 CYAA_YERPE - ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE)		UNCLASSIFIED	1038

7148	28483679 (4287, 4288)	Novel Protein sim. GBank gij1169207 sp P21705 DA82_YEAST - DAL82 PROTEIN		UNCLASSIFIED	1022
7149	20286427 (21059, 21060)	Novel Protein sim. GBank gij1169727 sp P44948 FPG_HAEIN - FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (FAPY-DNA GLYCOSYLASE)		UNCLASSIFIED	1034
7150	79238793 (295, 296)	Novel Protein sim. GBank gij1169843 sp P43574 GAT1_YEAST - GAT1 PROTEIN		UNCLASSIFIED	1003, 1008, 1017, 1022, 1026
7151	56026032 (18259, 18260)	Novel Protein sim. GBank gij1169870 sp P46959 GC14_YEAST - GCD14 PROTEIN		UNCLASSIFIED	1008, 1009
7152	80080574 (22845, 22846)	Novel Protein sim. GBank gij1170266 sp P44545 HFLC_HAEIN - HFLC PROTEIN		UNCLASSIFIED	1034
7153	11077845 (10793, 10794)	Novel Protein sim. GBank gij1170356 sp P42270 HPCG_ECOLI - 2-OXO- HEPTA-3-ENE-1,7-DIOIC ACID HYDRATASE (OHED HYDRATASE)		UNCLASSIFIED	1024
7154	80232907 (18639, 18640)	Novel Protein sim. GBank gij1170421 sp P46957 HUS2_YEAST - HUS2 PROTEIN		UNCLASSIFIED	1004, 1006, 1009, 1022
7155	65902299 (10708, 10710)	Novel Protein sim. GBank gij1170500 sp P44323 IF2_HAEIN - TRANSLATION INITIATION FACTOR IF-2		UNCLASSIFIED	1023
7156	85817675 (13327, 13328)	Novel Protein sim. GBank gij1170546 sp P44851 ILVD_HAEIN - DIHYDROXY-ACID DEHYDRATASE (DAD)		UNCLASSIFIED	1019
7157	27367613 (19653, 19654)	Novel Protein sim. GBank gij1170927 sp P45131 MET2_HAEIN - PUTATIVE HOMOSERINE O-ACETYLTRANSFERASE (HOMOSERINE O-TRANS-ACETYLASE)		UNCLASSIFIED	1017

7158	79111435 (5789, 5790)	Novel Protein sim. GBank gil1170950 sp P43638 MHP1_YEAST - MAP-HOMOLOGOUS PROTEIN 1		UNCLASSIFIED	1022, 1023
7159	27963648 (15965, 15966)	Novel Protein sim. GBank gil1170950 sp P43638 MHP1_YEAST - MAP-HOMOLOGOUS PROTEIN 1		UNCLASSIFIED	1034
7160	79598816 (4823, 4824)	Novel Protein sim. GBank gil1172447 sp P43751 PFLA_HAEIN - PYRUVATE FORMATE-LYASE 1 ACTIVATING ENZYME		UNCLASSIFIED	1003
7161	78407452 (22743, 22744)	Novel Protein sim. GBank gil1172509 sp P42257 PILJ_PSEAE - PILJ PROTEIN		UNCLASSIFIED	1005
7162	28393442 (12165, 12166)	Novel Protein sim. GBank gil1172551 sp P41812 POP1_YEAST - RNASES P/MRP PROTEIN POP1		UNCLASSIFIED	1008
7163	20296014 (7261, 7262)	Novel Protein sim. GBank gil1172766 sp P80210 PURA_YEAST - ADENYLOSUCCINATE SYNTHETASE (IMP--ASPARTATE LIGASE)		UNCLASSIFIED	1034
7164	80065893 (19477, 19478)	Novel Protein sim. GBank gil1172766 sp P80210 PURA_YEAST - ADENYLOSUCCINATE SYNTHETASE (IMP--ASPARTATE LIGASE)		UNCLASSIFIED	1003, 1004, 1006, 1017, 1039
7165	80503242 (19931, 19932)	Novel Protein sim. GBank gil1172803 sp P43123 QR1_YEAST - HYPOTHETICAL 53.5 KD PROTEIN IN PHO2-POL3 INTERGENIC REGION		UNCLASSIFIED	1012
7166	80218225 (1125, 1126)	Novel Protein sim. GBank gil1172804 sp P43124 QR2_YEAST - HYPOTHETICAL 46.1 KD PROTEIN IN PHO2-POL3 INTERGENIC REGION		UNCLASSIFIED	1004, 1006, 1010, 1017, 1022, 1026, 1034, 1038, 1044
7167	5280127 (19035, 19036)	Novel Protein sim. GBank gil117289 sp P18886 CPT2_RAT - MITOCHONDRIAL CARNITINE O-PALMITOYLTRANSFERASE II PRECURSOR (CPT II)		UNCLASSIFIED	1058

7168	71108523 (22709, 22710)	Novel Protein sim. GBank gil1173039 sp P42766 RL35_HUMAN - 60S RIBOSOMAL PROTEIN L35		UNCLASSIFIED	1029, 1046
7169	29683199 (625, 626)	Novel Protein sim. GBank gil1173375 sp P45978 SCD6_YEAST - SCD6 PROTEIN		UNCLASSIFIED	1009
7170	32548188 (13901, 13902)	Novel Protein sim. GBank gil1173451 sp P11994 SM50_STRPU - 50 KD SPICULE MATRIX PROTEIN PRECURSOR		UNCLASSIFIED	1006
7171	49522032 (17851, 17852)	Novel Protein sim. GBank gil1174092 (U43360) - reverse transcriptase [Peromyscus maniculatus]		UNCLASSIFIED	1040
7172	87447974 (15987, 15988)	Novel Protein sim. GBank gil1174160 (U44130) - p58 [Xenopus laevis]		UNCLASSIFIED	1025
7173	27968140 (19903, 19904)	Novel Protein sim. GBank gil1174538 sp P43831 SYQ_HAEIN - GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS)		UNCLASSIFIED	1006
7174	13086487 (20345, 20346)	Novel Protein sim. GBank gil1174661 sp P44594 TGT_HAEIN - QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA- GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)		UNCLASSIFIED	1027, 1031
7175	77520895 (20251, 20252)	Novel Protein sim. GBank gil1174934 sp P44042 VACJ_HAEIN - VACJ LIPOPROTEIN HOMOLOG PRECURSOR		UNCLASSIFIED	1049
7176	79639238 (11427, 11428)	Novel Protein sim. GBank gil1175322 sp P44917 Y883_HAEIN - HYPOTHETICAL PROTEIN HI0883		UNCLASSIFIED	1038
7177	30168195 (8481, 8482)	Novel Protein sim. GBank gil1175468 sp Q09800 YAA7_SCHPO - HYPOTHETICAL 47.3 KD PROTEIN C22G7.07C IN CHROMOSOME I		UNCLASSIFIED	1030
7178	79180227 (18737, 18738)	Novel Protein sim. GBank gil1175542 sp P44123 YB90_HAEIN - HYPOTHETICAL PROTEIN HI1190		UNCLASSIFIED	1022, 1031

7179	10183952 (13035, 13036)	Novel Protein sim. GBank gil1175687 sp P44732 ORDL_HAEIN - PROBABLE OXIDOREDUCTASE ORDL		UNCLASSIFIED	1003
7180	30656662 (3149, 3150)	Novel Protein sim. GBank gil1175772 sp P45244 YDJA_HAEIN - HYPOTHETICAL PROTEIN HI1542		UNCLASSIFIED	1026
7181	78741684 (13913, 13914)	Novel Protein sim. GBank gil1175777 sp P44176 YCIV_HAEIN - HYPOTHETICAL PROTEIN HI1400		UNCLASSIFIED	1008, 1039
7182	17936929 (1761, 1762)	Novel Protein sim. GBank gil1175791 sp P44189 YE18_HAEIN - HYPOTHETICAL PROTEIN HI1418		UNCLASSIFIED	1008, 1031
7183	25310980 (15681, 15682)	Novel Protein sim. GBank gil1175890 sp P44250 YCFW_HAEIN - HYPOTHETICAL PROTEIN HI1548		UNCLASSIFIED	1003
7184	79875270 (6713, 6714)	Novel Protein sim. GBank gil1175934 sp P43571 YFC5_YEAST - HYPOTHETICAL 117.8 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION		UNCLASSIFIED	1001, 1003, 1027
7185	78676588 (4449, 4450)	Novel Protein sim. GBank gil1175939 sp P43567 YFD0_YEAST - HYPOTHETICAL 41.9 KD PROTEIN IN HAC1-CAK1 INTERGENIC REGION		UNCLASSIFIED	1017
7186	39547846 (2439, 2440)	Novel Protein sim. GBank gil1175940 sp P43566 YFD2_YEAST - HYPOTHETICAL 12.4 KD PROTEIN IN RIM15-HAC1 INTERGENIC REGION		UNCLASSIFIED	1006
7187	27356171 (1747, 1748)	Novel Protein sim. GBank gil1175989 sp P43597 YFI6_YEAST - HYPOTHETICAL 137.7 KD PROTEIN IN UGS1-FAB1 INTERGENIC REGION		UNCLASSIFIED	1026
7188	56651079 (14131, 14132)	Novel Protein sim. GBank gil1176004 sp P43603 YFJ4_YEAST - HYPOTHETICAL 40.4 KD PROTEIN IN PES4-HIS2 INTERGENIC REGION		UNCLASSIFIED	1003, 1008, 1009, 1022, 1026

7189	20746548 (6611, 6612)	Novel Protein sim. GBank gil1176006 sp P43605 YFJ7_YEAST - HYPOTHETICAL 31.8 KD PROTEIN IN HIS2- CDC14 INTERGENIC REGION		UNCLASSIFIED	1022
7190	80435774 (14817, 14818)	Novel Protein sim. GBank gil1176008 sp P44568 RIMM_HAEIN - 16S RRNA PROCESSING PROTEIN RIMM		UNCLASSIFIED	1038
7191	56317997 (13421, 13422)	Novel Protein sim. GBank gil1176046 sp P44278 YG26_HAEIN - HYPOTHETICAL PROTEIN H1626		UNCLASSIFIED	1022
7192	20466513 (7007, 7008)	Novel Protein sim. GBank gil1176050 sp P42937 YG4E_YEAST - HYPOTHETICAL 17.2 KD PROTEIN IN PCT1- ADE3 INTERGENIC REGION		UNCLASSIFIED	1010
7193	78759653 (16413, 16414)	Novel Protein sim. GBank gil1176074 sp P46949 YG4A_YEAST - HYPOTHETICAL 90.8 KD PROTEIN IN RRP41- SNG1 INTERGENIC REGION		UNCLASSIFIED	1017
7194	79761150 (19941, 19942)	Novel Protein sim. GBank gil1176281 sp P46852 YHHW_ECOLI - HYPOTHETICAL 26.3 KD PROTEIN IN GNTR- GGT INTERGENIC REGION (F231)		UNCLASSIFIED	1008
7195	80234391 (22605, 22606)	Novel Protein sim. GBank gil1176338 sp P40355 YJ31_YEAST - HYPOTHETICAL 108.4 KD PROTEIN IN CBF1- NTA1 INTERGENIC REGION		UNCLASSIFIED	1001, 1004, 1006, 1016, 1022
7196	13504992 (11759, 11760)	Novel Protein sim. GBank gil1176356 sp P47039 YJG0_YEAST - HYPOTHETICAL AMINOTRANSFERASE YJL060W		UNCLASSIFIED	1004
7197	80099680 (11999, 12000)	Novel Protein sim. GBank gil1176475 sp P40358 YJH3_YEAST - HYPOTHETICAL 80.4 KD PROTEIN IN SMC3- MRPL8 INTERGENIC REGION		UNCLASSIFIED	1001, 1017, 1034
7198	11067395 (1309, 1310)	Novel Protein sim. GBank gil1176480 sp P44453 YJTT_HAEIN - HYPOTHETICAL PROTEIN H10012		UNCLASSIFIED	1004

7199	11093482 (20603, 20604)	Novel Protein sim. GBank gi 1176489 sp P42945 YJK9_YEAST - HYPOTHETICAL 200.0 KD PROTEIN IN GZF3- IME2 INTERGENIC REGION		UNCLASSIFIED	1022
7200	29457799 (1865, 1866)	Novel Protein sim. GBank gi 1176580 sp P42836 YN66_YEAST - HYPOTHETICAL 39.2 KD PROTEIN IN EGT2- KRE1 INTERGENIC REGION		UNCLASSIFIED	1009
7201	79174739 (22571, 22572)	Novel Protein sim. GBank gi 1176580 sp P42836 YN66_YEAST - HYPOTHETICAL 39.2 KD PROTEIN IN EGT2- KRE1 INTERGENIC REGION		UNCLASSIFIED	1024, 1026
7202	27837785 (15707, 15708)	Novel Protein sim. GBank gi 1176586 sp P42842 YN53_YEAST - HYPOTHETICAL 102.3 KD PROTEIN IN DAL82- RFA2 INTERGENIC REGION		UNCLASSIFIED	1006
7203	80212686 (4505, 4506)	Novel Protein sim. GBank gi 1176623 sp P41846 YO96_CAEEL - HYPOTHETICAL 93.9 KD PROTEIN T20B12.6 IN CHROMOSOME III		UNCLASSIFIED	1044
7204	24133335 (1923, 1924)	Novel Protein sim. GBank gi 1176823 sp P45301 YRAP_HAEIN - HYPOTHETICAL PROTEIN HI1658 PRECURSOR		UNCLASSIFIED	1003, 1023
7205	11397882 (17423, 17424)	Novel Protein sim. GBank gi 1176909 sp Q09825 YS8A_CAEEL - HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME II		UNCLASSIFIED	1006
7206	80190649 (14477, 14478)	Novel Protein sim. GBank gi 1176918 sp P24089 YSY2_YEAST - HYPOTHETICAL 137.7 KD PROTEIN IN SUBTELOMERIC Y' REPEAT REGION OF CHR XV (ORF 2)		UNCLASSIFIED	1004, 1006, 1008, 1009, 1022, 1024, 1029, 1034, 1038, 1058
7207	30652882 (20641, 20642)	Novel Protein sim. GBank gi 1176986 sp P42413 IOLB_BACSU - IOLB PROTEIN		UNCLASSIFIED	1022

7208	27830775 (20961, 20962)	Novel Protein sim. GBank gil1176986 sp P42413 IOLB_BACSU - IOLB PROTEIN		UNCLASSIFIED	1004
7209	80256730 (14165, 14166)	Novel Protein sim. GBank gil1181619 dbj BAA11565 - (D82364) a variant of TSC-22 [Gallus gallus]		UNCLASSIFIED	1022, 1034, 1037
7210	79444180 (16127, 16128)	Novel Protein sim. GBank gil1181619 dbj BAA11565 - (D82364) a variant of TSC-22 [Gallus gallus]		UNCLASSIFIED	1022, 1030, 1034, 1040
7211	20432745 (5255, 5256)	Novel Protein sim. GBank gil118302 sp P09890 DCDA_CORGL - DIAMINOPIMELATE DECARBOXYLASE (DAP DECARBOXYLASE)		UNCLASSIFIED	1024
7212	99417275 (12459, 12470)	Novel Protein sim. GBank gil119110 sp P03211 EBN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	1001, 1004, 1017, 1025, 1029, 1034, 1037, 1038, 1054
7213	80039105 (2187, 2188)	Novel Protein sim. GBank gil119111 sp P12978 EBN2_EBV - EBNA-2 NUCLEAR PROTEIN		UNCLASSIFIED	1037, 1058
7214	94294597 (8853, 8854)	Novel Protein sim. GBank gil119168 sp P09445 EF2_CRIGR - ELONGATION FACTOR 2 (EF-2)		UNCLASSIFIED	1024, 1026
7215	65484411 (4887, 4888)	Novel Protein sim. GBank gil119712 sp P14918 EXTN_MAIZE - EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN)		UNCLASSIFIED	1038
7216	79763392 (1897, 1898)	Novel Protein sim. GBank gil121058 sp P12754 E2BD_YEAST - TRANSLATION INITIATION FACTOR EIF-2B DELTA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR) (GUANINE NUCLEOTIDE EXCHANGE FACTOR SUBUNIT GCD2) (GCD COMPLEX SUBUNIT GCD2)		UNCLASSIFIED	1023

7217	87892844 (11937, 11938)	Novel Protein sim. GBank gil121472 sp P04706 GLU2_MAIZE - GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)		UNCLASSIFIED	1007, 1017, 1023, 1025, 1039
7218	11391492 (449, 450)	Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE- RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	1010
7219	79444757 (2145, 2146)	Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE- RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	1034
7220	11594422 (2699, 2700)	Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE- RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	1022
7221	79436235 (3639, 3640)	Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE- RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	1006
7222	28380726 (4207, 4208)	Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE- RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	1008
7223	11616471 (5917, 5918)	Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE- RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	1024
7224	11614608 (6171, 6172)	Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE- RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	1024
7225	80402888 (6533, 6534)	Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE- RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	1010, 1029, 1034

7226	46772992 (6635, 6636)	Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE- RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	1042
7227	79444618 (10919, 10920)	Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE- RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	1022
7228	95292713 (11687, 11688)	Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE- RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	1010, 1024
7229	11399702 (14119, 14120)	Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE- RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	1022
7230	8517613 (14955, 14956)	Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE- RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	1034
7231	11613962 (15533, 15534)	Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE- RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	1024
7232	79440943 (19479, 19480)	Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE- RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	1024
7233	19539975 (20555, 20556)	Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE- RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	1010
7234	79440440 (21049, 21050)	Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE- RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	1010

7235	91226916 (21705, 21706)	Novel Protein sim. GBank gij123530 sp P04929 HRPX_PLALO - HISTIDINE- RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	1010
7236	17902942 (22671, 22672)	Novel Protein sim. GBank gij123530 sp P04929 HRPX_PLALO - HISTIDINE- RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	1025
7237	13506251 (22925, 22926)	Novel Protein sim. GBank gij123530 sp P04929 HRPX_PLALO - HISTIDINE- RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	1034
7238	9535094 (2543, 2544)	Novel Protein sim. GBank gij125388 sp P22313 KHR1_YEAST - KILLER TOXIN KHR PRECURSOR (KILLER OF HEAT RESISTANT)		UNCLASSIFIED	1006
7239	16304862 (5891, 5892)	Novel Protein sim. GBank gij125388 sp P22313 KHR1_YEAST - KILLER TOXIN KHR PRECURSOR (KILLER OF HEAT RESISTANT)		UNCLASSIFIED	1024
7240	55007200 (13511, 13512)	Novel Protein sim. GBank gij126295 sp P08547 LIN1_HUMAN - LINE-1 REVERSE TRANSCRIPTASE HOMOLOG		UNCLASSIFIED	1019
7241	39520725 (21799, 21800)	Novel Protein sim. GBank gij126295 sp P08547 LIN1_HUMAN - LINE-1 REVERSE TRANSCRIPTASE HOMOLOG		UNCLASSIFIED	1010
7242	11100579 (22261, 22262)	Novel Protein sim. GBank gij126652 sp P25310 LYCM_STRGL - LYSOZYME M1 PRECURSOR (1,4-BETA-N- ACETYLMURAMIDASE M1)		UNCLASSIFIED	1006
7243	66490095 (14335, 14336)	Novel Protein sim. GBank gij126725 sp P21139 MAN1_RAT - ALPHA- MANNOSIDASE (ALPHA-D-MANNOSIDE MANNOHYDROLASE)		UNCLASSIFIED	1010, 1029

7244	17898280 (2465, 2466)	Novel Protein sim. GBank gil126923 sp P22412 MDP1_PIG - MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL DIPEPTIDASE) (RDP)		UNCLASSIFIED	1023
7245	9862729 (11903, 11904)	Novel Protein sim. GBank gil126980 sp P16523 MER1_YEAST - MEIOTIC RECOMBINATION 1 PROTEIN		UNCLASSIFIED	1008
7246	80237292 (9585, 9586)	Novel Protein sim. GBank gil127028 sp P15807 MET8_YEAST - MET8 PROTEIN		UNCLASSIFIED	1006, 1008, 1024, 1034, 1054
7247	80238451 (12975, 12976)	Novel Protein sim. GBank gil127091 sp P27705 MIG1_YEAST - REGULATORY PROTEIN MIG1 (REGULATORY PROTEIN CAT4)		UNCLASSIFIED	1006, 1008, 1010, 1022, 1023, 1024, 1031
7248	97989906 (13185, 13186)	Novel Protein sim. GBank gil128399 sp P14743 NMT_YEAST - GLYCYLPEPTIDE N- TETRADECANOYLTRANSFERASE (PEPTIDE N- MYRISTOYLTRANSFERASE) (MYRISTOYL- COA:PROTEIN N-MYRISTOYLTRANSFERASE) (NMT)		UNCLASSIFIED	1004, 1008, 1009, 1010, 1022, 1024, 1025, 1026, 1031, 1038
7249	35933517 (17737, 17738)	Novel Protein sim. GBank gil128853 sp P25284 NUEM_NEUCR - NADH- UBIQUINONE OXIDOREDUCTASE 40 KD SUBUNIT PRECURSOR (COMPLEX I-40KD) (CI- 40KD)		UNCLASSIFIED	1053
7250	78764791 (4289, 4290)	Novel Protein sim. GBank gil1293734 (U55021) - O3635p [Saccharomyces cerevisiae]		UNCLASSIFIED	1003, 1044
7251	99393009 (13279, 13280)	Novel Protein sim. GBank gil1293835 (U56965) - C15H9.5 gene product [Caenorhabditis elegans]		UNCLASSIFIED	1010, 1043
7252	80309285 (2785, 2786)	Novel Protein sim. GBank gil129849 sp P10355 PT22_YEAST - PET122 PROTEIN PRECURSOR		UNCLASSIFIED	1003, 1008, 1010, 1017, 1022, 1027, 1029, 1031

7253	78780743 (20515, 20516)	Novel Protein sim. GBank gil130158 sp P05066 PHR_YEAST - DEOXYRIBODIPYRIMIDINE PHOTOLYASE PRECURSOR (DNA PHOTOLYASE) (PHOTOREACTIVATING ENZYME)		UNCLASSIFIED	1009
7254	25139051 (3893, 3894)	Novel Protein sim. GBank gil130807 sp P19735 PR06_YEAST - PRE-MRNA SPLICING FACTOR PRP6		UNCLASSIFIED	1003, 1024
7255	78770835 (5673, 5674)	Novel Protein sim. GBank gil130899 sp P20457 PRI2_YEAST - DNA PRIMASE LARGE SUBUNIT (DNA PRIMASE 58 KD SUBUNIT) (P58)		UNCLASSIFIED	1026, 1039
7256	57301086 (15045, 15046)	Novel Protein sim. GBank gil131421 sp P22355 PSPB_RAT - PULMONARY SURFACTANT-ASSOCIATED PROTEIN B PRECURSOR (SP-B) (PULMONARY SURFACTANT-ASSOCIATED PROTEOLIPID SPL(PHE))		UNCLASSIFIED	1004, 1010, 1034
7257	10064064 (11539, 11540)	Novel Protein sim. GBank gil131490 sp P20966 PTFB_ECOLI - PTS SYSTEM, FRUCTOSE-SPECIFIC IIBC COMPONENT (EIIBC-FRU) (FRUCTOSE- PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EII-FRU)		UNCLASSIFIED	1012
7258	87453399 (21053, 21054)	Novel Protein sim. GBank gil131605 sp P25822 PUM_DROME - MATERNAL PUMILIO PROTEIN		UNCLASSIFIED	1025
7259	10094270 (11327, 11328)	Novel Protein sim. GBank gil131653 sp P25502 PUT3_YEAST - PROLINE UTILIZATION TRANS-ACTIVATOR		UNCLASSIFIED	1038
7260	85525890 (11763, 11764)	Novel Protein sim. GBank gil132278 sp P03047 REGO_LAMBD - ANTITERMINATION PROTEIN Q		UNCLASSIFIED	1049

7261	82782500 (1263, 1264)	Novel Protein sim. GBank gil132339 sp P03872 REP2_YEAST - TRANS- ACTING FACTOR C (REP2) (PROTEIN CHARLIE)		UNCLASSIFIED	1044
7262	79860240 (1935, 1936)	Novel Protein sim. GBank gil133144 sp P25299 RN15_YEAST - MRNA 3'- END PROCESSING PROTEIN RNA15		UNCLASSIFIED	1017
7263	85531559 (16005, 16006)	Novel Protein sim. GBank gil1335205 emb CAA36480 - (X52235) ORFII [Homo sapiens]		UNCLASSIFIED	1038
7264	39586996 (749, 750)	Novel Protein sim. GBank gil133950 dbj BAA12741 - (D85230) large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]		UNCLASSIFIED	1006, 1024, 1034
7265	20633647 (2989, 2990)	Novel Protein sim. GBank gil134196 sp P23832 SAMB_SALTY - SAMB PROTEIN		UNCLASSIFIED	1004
7266	80502023 (14377, 14378)	Novel Protein sim. GBank gil134221 sp P20606 SAR1_YEAST - GTP- BINDING PROTEIN SAR1		UNCLASSIFIED	1004, 1006, 1008, 1009, 1012, 1017, 1022, 1024, 1025, 1026, 1027, 1034, 1038, 1039, 1058
7267	38280077 (13529, 13530)	Novel Protein sim. GBank gil134506 sp P06700 SIR2_YEAST - REGULATORY PROTEIN SIR2 (SILENT INFORMATION REGULATOR 2)		UNCLASSIFIED	1008, 1022
7268	87453059 (19407, 19408)	Novel Protein sim. GBank gil1346104 sp P49083 GBA1_ORYSA - GUANINE NUCLEOTIDE-BINDING PROTEIN ALPHA-1 SUBUNIT (GP-ALPHA-1)		UNCLASSIFIED	1025
7269	95198855 (2389, 2390)	Novel Protein sim. GBank gil1346340 sp P47135 JSN1_YEAST - JSN1 PROTEIN		UNCLASSIFIED	1008, 1029, 1044

7270	57301782 (2929, 2930)	Novel Protein sim. GBank gi 1346340 sp P47135 JSN1_YEAST - JSN1 PROTEIN		UNCLASSIFIED	1004, 1022, 1034
7271	28801598 (8563, 8564)	Novel Protein sim. GBank gi 1346647 sp P49687 N145_YEAST - NUCLEOPORIN NUP145 (NUCLEAR PORE PROTEIN NUP145)		UNCLASSIFIED	1017, 1024
7272	80079596 (13885, 13886)	Novel Protein sim. GBank gi 1346722 sp P49022 PIP_LACLA - PHAGE INFECTION PROTEIN		UNCLASSIFIED	1034
7273	11776932 (15913, 15914)	Novel Protein sim. GBank gi 1346916 sp P12283 PURA_ECOLI - ADENYLOSUCCINATE SYNTHETASE (IMP-- ASPARTATE LIGASE)		UNCLASSIFIED	1006
7274	29014276 (15647, 15648)	Novel Protein sim. GBank gi 134780 sp P14328 SP96_DICDI - SPORE COAT PROTEIN SP96		UNCLASSIFIED	1030
7275	47654653 (18403, 18404)	Novel Protein sim. GBank gi 134760 sp P14328 SP96_DICDI - SPORE COAT PROTEIN SP96		UNCLASSIFIED	1029, 1053
7276	65685543 (10481, 10482)	Novel Protein sim. GBank gi 134781 sp P23201 SPA2_YEAST - SPA2 PROTEIN		UNCLASSIFIED	1049
7277	81743047 (14507, 14508)	Novel Protein sim. GBank gi 134853 sp P27692 SPT5_YEAST - TRANSCRIPTION INITIATION PROTEIN SPT5		UNCLASSIFIED	1004, 1006, 1012, 1017, 1024, 1034, 1036, 1039, 1054
7278	65460683 (9065, 9066)	Novel Protein sim. GBank gi 134854 sp P23615 SPT6_YEAST - TRANSCRIPTION INITIATION PROTEIN SPT6		UNCLASSIFIED	1054
7279	78926555 (22527, 22528)	Novel Protein sim. GBank gi 134856 sp P09139 SPYA_RAT - SERINE-- PYRUVATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (SPT) (ALANINE--GLYOXYLATE AMINOTRANSFERASE) (AGT)		UNCLASSIFIED	1008

7280	82452137 (7861, 7862)	Novel Protein sim. GBank gil134935 sp P11972 SST2_YEAST - SST2 PROTEIN		UNCLASSIFIED	1001, 1004, 1006, 1008, 1010, 1012, 1017, 1021, 1022, 1023, 1024, 1031, 1034, 1038, 1039, 1044, 1054
7281	11077318 (6707, 6708)	Novel Protein sim. GBank gil1351412 sp P26700 VPH_BPP2 - PROBABLE TAIL FIBRE PROTEIN (GPH)		UNCLASSIFIED	1004, 1008
7282	20458563 (19733, 19734)	Novel Protein sim. GBank gil1351728 sp Q10110 YAQA_SCHPO - HYPOTHETICAL 68.6 KD PROTEIN C18G6.10C IN CHROMOSOME I		UNCLASSIFIED	1010
7283	39456271 (6425, 6426)	Novel Protein sim. GBank gil135175 sp P18255 SYT1_BACSU - THREONYL TRNA SYNTHETASE 1 (THREONINE--TRNA LIGASE) (THRRS)		UNCLASSIFIED	1006
7284	94668466 (6775, 6776)	Novel Protein sim. GBank gil1351819 sp P48234 YG3J_YEAST - HYPOTHETICAL 81.7 KD PROTEIN IN MOL1- NAT2 INTERGENIC REGION		UNCLASSIFIED	1024, 1034
7285	27836711 (5477, 5478)	Novel Protein sim. GBank gil1351825 sp P39927 YG3Q_YEAST - HYPOTHETICAL 47.0 KD PROTEIN IN CYS4- PEM1 INTERGENIC REGION		UNCLASSIFIED	1006
7286	78387082 (18149, 18150)	Novel Protein sim. GBank gil1352839 sp P06921 VE2_HPV05 - REGULATORY PROTEIN E2		UNCLASSIFIED	1026
7287	78778316 (20623, 20624)	Novel Protein sim. GBank gil1352879 sp P47108 YJ11_YEAST - HYPOTHETICAL 135.1 KD PROTEIN IN GEF1- NUP85 INTERGENIC REGION		UNCLASSIFIED	1026

7288	79831931 (1713, 1714)	Novel Protein sim. GBank gil1352880 sp P47110 YJ13_YEAST - HYPOTHETICAL 40.3 KD PROTEIN IN NUP85- SSC1 INTERGENIC REGION		UNCLASSIFIED	1008, 1022, 1044
7289	56470631 (13149, 13150)	Novel Protein sim. GBank gil1352890 sp P47123 YJ44_YEAST - HYPOTHETICAL 24.3 KD PROTEIN IN PEM2- HOC1 INTERGENIC REGION		UNCLASSIFIED	1017
7290	78898911 (15183, 15184)	Novel Protein sim. GBank gil1352911 sp P47147 YJ80_YEAST - HYPOTHETICAL 80.2 KD PROTEIN IN CPA2- NNF1 INTERGENIC REGION		UNCLASSIFIED	1017
7291	79113310 (19465, 19466)	Novel Protein sim. GBank gil1352911 sp P47147 YJ80_YEAST - HYPOTHETICAL 80.2 KD PROTEIN IN CPA2- NNF1 INTERGENIC REGION		UNCLASSIFIED	1003
7292	65442574 (1821, 1822)	Novel Protein sim. GBank gil1352912 sp P47148 YJ81_YEAST - HYPOTHETICAL 32.2 KD PROTEIN IN CPA2- NNF1 INTERGENIC REGION		UNCLASSIFIED	1049
7293	28794827 (993, 994)	Novel Protein sim. GBank gil1352936 sp P47171 YJ9H_YEAST - HYPOTHETICAL 191.7 KD PROTEIN IN HOM6- PMT4 INTERGENIC REGION		UNCLASSIFIED	1022
7294	17676882 (10381, 10382)	Novel Protein sim. GBank gil1352943 sp P47178 YJ9O_YEAST - HYPOTHETICAL 29.5 KD PROTEIN IN BAT2- DAL5 INTERGENIC REGION PRECURSOR		UNCLASSIFIED	1039
7295	78791899 (4659, 4660)	Novel Protein sim. GBank gil1352944 sp P47179 YJ9P_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2- DAL5 INTERGENIC REGION PRECURSOR		UNCLASSIFIED	1009
7296	20696279 (18055, 18056)	Novel Protein sim. GBank gil1352952 sp P47080 YJ47_YEAST - HYPOTHETICAL 11.9 KD PROTEIN IN CCT8- CTK2 INTERGENIC REGION		UNCLASSIFIED	1006

7297	8498789 (11183, 11184)	Novel Protein sim. GBank gil1352962 sp P47089 YJB9_YEAST - HYPOTHETICAL 72.4 KD PROTEIN IN PET130- CCT3 INTERGENIC REGION		UNCLASSIFIED	1022
7298	20446403 (4639, 4640)	Novel Protein sim. GBank gil1352981 sp P47046 YJF1_YEAST - HYPOTHETICAL 91.3 KD PROTEIN IN TDH1- MTR4 INTERGENIC REGION		UNCLASSIFIED	1004
7299	82114223 (659, 660)	Novel Protein sim. GBank gil1352995 sp P47031 YJ12_YEAST - HYPOTHETICAL 82.5 KD PROTEIN IN EXO70- ARP4 INTERGENIC REGION		UNCLASSIFIED	1004, 1016, 1024
7300	79186760 (14717, 14718)	Novel Protein sim. GBank gil1352995 sp P47031 YJ12_YEAST - HYPOTHETICAL 82.5 KD PROTEIN IN EXO70- ARP4 INTERGENIC REGION		UNCLASSIFIED	1006
7301	17894667 (847, 848)	Novel Protein sim. GBank gil1353043 sp P46982 YJS6_YEAST - HYPOTHETICAL 67.3 KD PROTEIN IN SWE1- ATP12 INTERGENIC REGION		UNCLASSIFIED	1017
7302	30383911 (4599, 4600)	Novel Protein sim. GBank gil1353050 sp P47086 YJY1_YEAST - HYPOTHETICAL 30.5 KD PROTEIN IN SPC1- ILV3 INTERGENIC REGION		UNCLASSIFIED	1034
7303	23295044 (4507, 4508)	Novel Protein sim. GBank gil1353083 sp P49017 COQ5_YEAST - UBIQUINONE BIOSYNTHESIS METHYLTRANSFERASE COQ5		UNCLASSIFIED	1003
7304	38277876 (8553, 8554)	Novel Protein sim. GBank gil1353105 sp P48563 YN37_YEAST - HYPOTHETICAL 186.8 KD PROTEIN IN CLA4- MID1 INTERGENIC REGION		UNCLASSIFIED	1009
7305	20285552 (12003, 12004)	Novel Protein sim. GBank gil13612 t5 pir S56581 - methyl-accepting chemotaxis protein I - Escherichia coli		UNCLASSIFIED	1034

7306	79866035 (10433, 10434)	Novel Protein sim. GBank gi 1363693 pir S58781 - probable membrane protein YDL196w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1022, 1038
7307	78372416 (10739, 10740)	Novel Protein sim. GBank gi 1363731 pir S59414 - hypothetical protein YLR455w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1039
7308	30642846 (7251, 7252)	Novel Protein sim. GBank gi 1363748 pir S59408 - probable membrane protein YLR440c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1022
7309	30615264 (9405, 9406)	Novel Protein sim. GBank gi 1363751 pir S59382 - hypothetical protein YLR417w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1009, 1026
7310	9884992 (18215, 18216)	Novel Protein sim. GBank gi 138595 sp P02845 VIT2_CHICK - VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LVI); PHOSVITIN (PV); LIPOVITELLIN II (LVII); YGP40]		UNCLASSIFIED	1008
7311	10095761 (17109, 17110)	Novel Protein sim. GBank gi 139232 sp P16753 VP40_HCMVA - CAPSID PROTEIN P40 (CONTAINS: ASSEMBLY (PROTEASE) AND CAPSID ASSEMBLY PROTEIN)		UNCLASSIFIED	1038
7312	27929979 (20013, 20014)	Novel Protein sim. GBank gi 1399965 (U62317) - hypothetical protein 384D8_6 [Homo sapiens]		UNCLASSIFIED	1006, 1010
7313	20464958 (19943, 19944)	Novel Protein sim. GBank gi 140025 sp P06567 DNAI_BACSU - PRIMOSOMAL PROTEIN DNAI		UNCLASSIFIED	1010
7314	29342129 (7141, 7142)	Novel Protein sim. GBank gi 140331 sp P25587 YCA5_YEAST - HYPOTHETICAL 28.7 KD PROTEIN IN CWH36-PEL1 INTERGENIC REGION		UNCLASSIFIED	1022

7315	39547428 (14057, 14058)	Novel Protein sim. GBank gil140332 sp P25595 YCA6_YEAST - HYPOTHETICAL 12.5 KD PROTEIN IN CWH36- PEL1 INTERGENIC REGION		UNCLASSIFIED	1006
7316	9522648 (20733, 20734)	Novel Protein sim. GBank gil140338 sp P21367 YCAC_ECOLI - HYPOTHETICAL 23.1 KD PROTEIN IN DMSC- PFLA INTERGENIC REGION		UNCLASSIFIED	1003
7317	95293089 (3161, 3162)	Novel Protein sim. GBank gil140351 sp P25384 YCB9_YEAST - TRANSPOSON TY1-17 PROTEIN B		UNCLASSIFIED	1024
7318	27824104 (5711, 5712)	Novel Protein sim. GBank gil140372 sp P25569 YCD9_YEAST - HYPOTHETICAL 86.0 KD PROTEIN IN GLK1- SRO9 INTERGENIC REGION		UNCLASSIFIED	1024
7319	80478105 (22263, 22264)	Novel Protein sim. GBank gil140372 sp P25569 YCD9_YEAST - HYPOTHETICAL 86.0 KD PROTEIN IN GLK1- SRO9 INTERGENIC REGION		UNCLASSIFIED	1012, 1022
7320	17896104 (777, 778)	Novel Protein sim. GBank gil140380 sp P25576 YCE7_YEAST - HYPOTHETICAL 29.7 KD PROTEIN IN APA1/DTP-PDI1 INTERGENIC REGION		UNCLASSIFIED	1044
7321	6756409 (4849, 4850)	Novel Protein sim. GBank gil140477 sp P25353 YCR6_YEAST - HYPOTHETICAL 84.9 KD PROTEIN IN PMP1- FEN2 INTERGENIC REGION		UNCLASSIFIED	1022
7322	95294802 (6763, 6764)	Novel Protein sim. GBank gil140525 sp P25641 YCV8_YEAST - HYPOTHETICAL 49.3 KD PROTEIN IN SCC3 5'REGION		UNCLASSIFIED	1010, 1022, 1058
7323	25136226 (10049, 10050)	Novel Protein sim. GBank gil140544 emb CAA66080.1 - (X97449) primosomal protein N [Borrelia burgdorferi]		UNCLASSIFIED	1026

7324	20598718 (15705, 15706)	Novel Protein sim. GBank gil140687 sp P11666 YGG_B_ECOLI - HYPOTHETICAL 30.9 KD PROTEIN IN SBM-FBA INTERGENIC REGION (ORF 4) (F286)		UNCLASSIFIED	1053
7325	20617110 (20331, 20332)	Novel Protein sim. GBank gil140723 sp P25489 HRCA_BACSU - HEAT- INDUCIBLE TRANSCRIPTION REPRESSOR HRCA		UNCLASSIFIED	1004
7326	9644134 (21117, 21118)	Novel Protein sim. GBank gil140750 sp P25536 YHDE_ECOLI - HYPOTHETICAL 21.5 KD PROTEIN IN CAFA- MRED INTERGENIC REGION (ORFE)		UNCLASSIFIED	1039
7327	21434980 (22405, 22406)	Novel Protein sim. GBank gil141103 sp P11260 YO11_MOUSE - HYPOTHETICAL PROTEIN ORF-1137		UNCLASSIFIED	1024
7328	78103835 (3243, 3244)	Novel Protein sim. GBank gil141470 sp P19658 EX70_YEAST - 70 KD EXOCYST COMPLEX PROTEIN		UNCLASSIFIED	1036
7329	80234966 (14657, 14658)	Novel Protein sim. GBank gil141515 sp P25639 YCV1_YEAST - HYPOTHETICAL 65.0 KD PROTEIN IN PWP2- SUP61 INTERGENIC REGION		UNCLASSIFIED	1001, 1003, 1016, 1022
7330	79830278 (3163, 3164)	Novel Protein sim. GBank gil1460074 emb CAB01049 - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis]		UNCLASSIFIED	1039, 1049
7331	19885057 (8677, 8678)	Novel Protein sim. GBank gil1460074 emb CAB01049 - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis]		UNCLASSIFIED	1001
7332	24125719 (13983, 13984)	Novel Protein sim. GBank gil1469882 dbj BAA09771 - (D63484) The KIAA0150 gene product is novel. [Homo sapiens]		UNCLASSIFIED	1009
7333	79865185 (14059, 14060)	Novel Protein sim. GBank gil1497861 (U40587) - fiber gene product [Fowl adenovirus]		UNCLASSIFIED	1025

7334	65472599 (903, 904)	Novel Protein sim. GBank gij1524205[emb]CAB01993] - (Z79700) purH [Mycobacterium tuberculosis]		UNCLASSIFIED	1010, 1023
7335	8488433 (12359, 12360)	Novel Protein sim. GBank gij1552873[emb]CAB02469] - (Z80343) hypothetical protein Rv3790 [Mycobacterium tuberculosis]		UNCLASSIFIED	1024
7336	16395807 (10211, 10212)	Novel Protein sim. GBank gj1572819 (U70855) - similar to the RAS gene family [Caenorhabditis elegans]		UNCLASSIFIED	1017
7337	78747341 (12127, 12128)	Novel Protein sim. GBank gj1573895 (U32769) - conserved hypothetical protein [Haemophilus influenzae Rd]		UNCLASSIFIED	1022
7338	88083418 (9647, 9648)	Novel Protein sim. GBank gj1622787 (U47644) - Notch2 gene product [Feline leukemia virus]		UNCLASSIFIED	1008, 1054
7339	78700638 (2697, 2698)	Novel Protein sim. GBank gij1644232[dbj]BAA11082] - (D67066) N-WASP [Bos taurus]		UNCLASSIFIED	1017
7340	37003614 (2117, 2118)	Novel Protein sim. GBank gj1644457 (U72521) - neural variant mena+ protein [Mus musculus]		UNCLASSIFIED	1029
7341	78183445 (12563, 12564)	Novel Protein sim. GBank gij1648880[emb]CAB03669] - (Z81331) hypothetical protein Rv2840c [Mycobacterium tuberculosis]		UNCLASSIFIED	1029, 1053
7342	80069047 (3803, 3804)	Novel Protein sim. GBank gij1651952[dbj]BAA16878] - (D90901) precorrin methylase [Synechocystis sp.]		UNCLASSIFIED	1010, 1023
7343	80500859 (4009, 4010)	Novel Protein sim. GBank gij1652206[dbj]BAA17130] - (D90903) regulatory components of sensory transduction system [Synechocystis sp.]		UNCLASSIFIED	1006, 1012
7344	8050260 (14527, 14528)	Novel Protein sim. GBank gij1652750[dbj]BAA17669] - (D90908) transcriptional regulator [Synechocystis sp.]		UNCLASSIFIED	1004
7345	37034601 (1467, 1468)	Novel Protein sim. GBank gij1652893[dbj]BAA17811] - (D90909) hypothetical protein [Synechocystis sp.]		UNCLASSIFIED	1012

7346	88094359 (5937, 5938)	Novel Protein sim. GBank gil1653184 dbj BAA18100 - (D90911) hypothetical protein [Synnechocystis sp.]		UNCLASSIFIED	1010
7347	32436128 (19103, 19104)	Novel Protein sim. GBank gil1653325 dbj BAA18240 - (D90912) tynocyte protein cThy28kD [Synnechocystis sp.]		UNCLASSIFIED	1029
7348	82443430 (20183, 20184)	Novel Protein sim. GBank gil1653805 dbj BAA18716 - (D90916) hypothetical protein [Synnechocystis sp.]		UNCLASSIFIED	1001, 1012, 1022, 1023, 1034, 1044
7349	30658118 (5293, 5294)	Novel Protein sim. GBank gil1654108 (U11283) - RpoE homologue [Rhodobacter sphaeroides]		UNCLASSIFIED	1026
7350	20619990 (5613, 5614)	Novel Protein sim. GBank gil1655665 emb CAB03731 - (Z81368) hypothetical protein Rv2395 [Mycobacterium tuberculosis]		UNCLASSIFIED	1004, 1024
7351	95002716 (10637, 10638)	Novel Protein sim. GBank gil1655699 emb CAA69032 - (Y07752) pherophorin-S [Volvox carteri]		UNCLASSIFIED	1006
7352	70950672 (17639, 17640)	Novel Protein sim. GBank gil1655699 emb CAA69032 - (Y07752) pherophorin-S [Volvox carteri]		UNCLASSIFIED	1029
7353	25255880 (17699, 17700)	Novel Protein sim. GBank gil1657608 (U66846) - orf5 [Streptococcus pneumoniae]		UNCLASSIFIED	1008
7354	78743353 (4549, 4550)	Novel Protein sim. GBank gil1665817 dbj BAA13405 - (D87466) Similar to S. cerevisiae hypothetical protein L3111 (S59316) [Homo sapiens]		UNCLASSIFIED	1025, 1044
7355	18552821 (2487, 2488)	Novel Protein sim. GBank gil1666137 emb CAB05053 - (Z82098) hypothetical protein Rv3523 [Mycobacterium tuberculosis]		UNCLASSIFIED	1001
7356	78674147 (16331, 16332)	Novel Protein sim. GBank gil1666689 (U48363) - alpha-NAC, muscle-specific form gp220 [Mus musculus]		UNCLASSIFIED	1026
7357	37797730 (17479, 17480)	Novel Protein sim. GBank gil1673402 emb CAB04812 - (Z82044) hypothetical 54.4 kd protein [Bacillus subtilis]		UNCLASSIFIED	1012

7358	78707254 (15869, 15870)	Novel Protein sim. GBank gi 1679692 (U76205) - scavenger receptor class B type I [Rattus norvegicus]		UNCLASSIFIED	1008, 1022, 1026, 1039
7359	80054196 (14549, 14550)	Novel Protein sim. GBank gi 1684738[emb CAA70601] - (Y09452) Yed j hypothetical protein [Pseudomonas syringae]		UNCLASSIFIED	1004, 1024
7360	7533261 (2819, 2820)	Novel Protein sim. GBank gi 1688307 (U78556) - cisplatin resistance associated alpha protein [Homo sapiens]		UNCLASSIFIED	1058
7361	80082471 (15365, 15366)	Novel Protein sim. GBank gi 1694859[emb CAB05439] - (Z83018) hypothetical protein Rv2972c [Mycobacterium tuberculosis]		UNCLASSIFIED	1034
7362	37392439 (5241, 5242)	Novel Protein sim. GBank gi 1703228[sp P52893]ALAM_YEAST - PUTATIVE ALANINE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (GLUTAMIC--PYRUVIC TRANSAMINASE) (GPT) (GLUTAMIC--ALANINE TRANSAMINASE)		UNCLASSIFIED	1003, 1036
7363	79112104 (20729, 20730)	Novel Protein sim. GBank gi 1703440[sp P50275]ASE1_YEAST - ANAPHASE SPINDLE ELONGATION PROTEIN		UNCLASSIFIED	1017, 1039
7364	54530976 (1, 2)	Novel Protein sim. GBank gi 1705513[sp P47136]BUD4_YEAST - BUD SITE SELECTION PROTEIN BUD4		UNCLASSIFIED	1041
7365	17649323 (22135, 22136)	Novel Protein sim. GBank gi 1706001[sp P32074]COPG_YEAST - COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP)		UNCLASSIFIED	1017
7366	17295570 (7379, 7380)	Novel Protein sim. GBank gi 1706711[sp P53573]ETFA_BRAJA - ELECTRON TRANSFER FLAVOPROTEIN ALPHA-SUBUNIT (ALPHA-ETF) (ELECTRON TRANSFER FLAVOPROTEIN LARGE SUBUNIT) (ETFLS)		UNCLASSIFIED	1039

7367	27959424 (5985, 5986)	Novel Protein sim. GBank gil1706879 sp P50264 FMS1_YEAST - FMS1 PROTEIN		UNCLASSIFIED	1006
7368	20740759 (1103, 1104)	Novel Protein sim. GBank gil1706929 sp Q10969 FTSY_MYCTU - CELL DIVISION PROTEIN FTSY HOMOLOG		UNCLASSIFIED	1001, 1022
7369	8521650 (6381, 6382)	Novel Protein sim. GBank gil1707032 (U80445) - coded for by C. elegans cDNA yk13g5.3; coded for by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA yk65h8....		UNCLASSIFIED	1010
7370	21422954 (10085, 10086)	Novel Protein sim. GBank gil1707703 emb CAA695071 - (Y08256) orf c06024 [Sulfolobus solfataricus]		UNCLASSIFIED	1022, 1024, 1027, 1034
7371	80481749 (7733, 7734)	Novel Protein sim. GBank gil1707970 sp Q10379 GLNE_MYCTU - PROBABLE GLUTAMATE-AMMONIA-LIGASE ADENYLYLTRANSFERASE (GLUTAMINE-SYNTHETASE ADENYLYLTRANSFERASE) (ATASE)		UNCLASSIFIED	1006, 1010, 1012, 1024, 1026
7372	79954898 (3983, 3984)	Novel Protein sim. GBank gil1708869 sp P52691 LRRRA_SYNPT - PROBABLE TRANSCRIPTIONAL REGULATOR LRRRA		UNCLASSIFIED	1001
7373	13046995 (12565, 12566)	Novel Protein sim. GBank gil1708874 sp P52689 LTRA_KLEPN - PROBABLE TRANSCRIPTIONAL REGULATOR LTRA		UNCLASSIFIED	1024
7374	78469078 (19937, 19938)	Novel Protein sim. GBank gil1709285 sp P52965 NIFJ_SYN3 - PUTATIVE PYRUVATE-FLAVODOXIN OXIDOREDUCTASE		UNCLASSIFIED	1026
7375	80026646 (10841, 10842)	Novel Protein sim. GBank gil1709621 sp P51533 PDRA_YEAST - ATP-DEPENDENT PERMEASE PDR10		UNCLASSIFIED	1004, 1006, 1017

7376	11090572 (4213, 4214)	Novel Protein sim. GBank gil1709733 sp P51065 PPCK_STAAU - PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP)		UNCLASSIFIED	1006
7377	79888025 (12483, 12484)	Novel Protein sim. GBank gil1709751 sp P55174 PQQF_PSEFL - COENZYME PQQ SYNTHESIS PROTEIN F		UNCLASSIFIED	1003
7378	8500276 (22941, 22942)	Novel Protein sim. GBank gil1709753 sp P32523 PR19_YEAST - PRE- MRNA SPLICING FACTOR PRP19		UNCLASSIFIED	1004
7379	13041977 (7213, 7214)	Novel Protein sim. GBank gil1710106 sp Q10606 RFE_MYCTU - PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N- ACETYLGLUCOSAMINYLTRANSFERASE		UNCLASSIFIED	1024
7380	32297376 (14083, 14084)	Novel Protein sim. GBank gil1710216 (U79260) - unknown [Homo sapiens]		UNCLASSIFIED	1000
7381	80077389 (9745, 9746)	Novel Protein sim. GBank gil1710383 sp P46352 RIPX_BACSU - PROBABLE INTEGRASE/RECOMBINASE RIPX		UNCLASSIFIED	1034
7382	80223293 (773, 774)	Novel Protein sim. GBank gil1711345 sp P53012 SCS3_YEAST - SCS3 PROTEIN		UNCLASSIFIED	1003, 1008, 1024, 1031
7383	29347374 (1133, 1134)	Novel Protein sim. GBank gil1711392 sp P06701 SIR3_YEAST - REGULATORY PROTEIN SIR3 (SILENT INFORMATION REGULATOR 3)		UNCLASSIFIED	1022
7384	20731350 (18963, 18964)	Novel Protein sim. GBank gil1711396 sp P54867 SLG1_YEAST - SLG1 PROTEIN PRECURSOR		UNCLASSIFIED	1004
7385	80504082 (9335, 9336)	Novel Protein sim. GBank gil1711469 sp P54998 SOXC_RHOSO - DIBENZOTHIOPHENE DESULFURIZATION ENZYME C (DBT SULFUR DIOXYGENASE)		UNCLASSIFIED	1012

7386	80503589 (15415, 15416)	Novel Protein sim. GBank gi 1711497 sp P53541 SPO1_YEAST - SPORULATION PROTEIN SPO1		UNCLASSIFIED	1006, 1008, 1012, 1022, 1024
7387	79931391 (20455, 20456)	Novel Protein sim. GBank gi 1711619 sp P53628 SNFC_YEAST - TRANSCRIPTION REGULATORY PROTEIN SNF12 (SWI/SNF COMPLEX COMPONENT SWP73)		UNCLASSIFIED	1008, 1024
7388	78788083 (9721, 9722)	Novel Protein sim. GBank gi 171374 (M60415) - DAL81 [Saccharomyces cerevisiae]		UNCLASSIFIED	1009, 1022
7389	29203926 (8325, 8326)	Novel Protein sim. GBank gi 171483 (M59708) - sec21p [Saccharomyces cerevisiae]		UNCLASSIFIED	1008
7390	27842655 (6667, 6668)	Novel Protein sim. GBank gi 171596 (J04719) - D-fructose-6-phosphate amidotransferase (EC 2.6.1.16) [Saccharomyces cerevisiae]		UNCLASSIFIED	1006
7391	10224420 (6703, 6704)	Novel Protein sim. GBank gi 171666 (M33703) - Hex2 protein [Saccharomyces cerevisiae]		UNCLASSIFIED	1022, 1034
7392	20625793 (18135, 18136)	Novel Protein sim. GBank gi 171940 (M84455) - leucine zipper protein [Saccharomyces cerevisiae]		UNCLASSIFIED	1023, 1034
7393	30658154 (11121, 11122)	Novel Protein sim. GBank gi 172076 (M88605) - contains Cys-4 zinc-finger, resembles erythroid transcription factor GATA-1; ORF [Saccharomyces cerevisiae]		UNCLASSIFIED	1026
7394	11135839 (13607, 13608)	Novel Protein sim. GBank gi 172081 (M88607) - H1-like protein, high in lys and ser; ORF 2 [Saccharomyces cerevisiae]		UNCLASSIFIED	1034
7395	79564830 (16607, 16608)	Novel Protein sim. GBank gi 172094 (M36822) - SIN3 open reading frame [Saccharomyces cerevisiae]		UNCLASSIFIED	1001, 1008, 1022
7396	7431475 (2059, 2060)	Novel Protein sim. GBank gi 172096 (M90688) - polyA nuclease [Saccharomyces cerevisiae]		UNCLASSIFIED	1058
7397	78459988 (6569, 6570)	Novel Protein sim. GBank gi 1723026 sp Q10897 Y05L_MYCTU - HYPOTHETICAL 70.4 KD PROTEIN CY251.21		UNCLASSIFIED	1026

7398	20370183 (13393, 13394)	Novel Protein sim. GBank gij1723119 sp P53990 Y174_HUMAN - HYPOTHETICAL PROTEIN KIAA0174		UNCLASSIFIED	1024
7399	78770076 (20677, 20678)	Novel Protein sim. GBank gij1723183 sp P39734 YAC8_YEAST - HYPOTHETICAL 58.8 KD PROTEIN IN MYO4- DRS2 INTERGENIC REGION		UNCLASSIFIED	1003, 1017, 1034, 1039, 1044
7400	10206877 (16945, 16946)	Novel Protein sim. GBank gij1723189 sp P39731 YADA_YEAST - HYPOTHETICAL 33.2 KD PROTEIN IN PYK1- SNC1 INTERGENIC REGION		UNCLASSIFIED	1025
7401	86685530 (13541, 13542)	Novel Protein sim. GBank gij1723279 sp Q10211 YAY3_SCHPO - HYPOTHETICAL 74.5 KD PROTEIN C4H3.03C IN CHROMOSOME I		UNCLASSIFIED	1029
7402	7889607 (16101, 16102)	Novel Protein sim. GBank gij1723566 sp Q10479 YDF7_SCHPO - PUTATIVE GLUCOSYLTRANSFERASE C17C9.07		UNCLASSIFIED	1017
7403	80216490 (20481, 20482)	Novel Protein sim. GBank gij1723647 sp P53209 YG1A_YEAST - HYPOTHETICAL 22.2 KD PROTEIN IN MSB2- UGA1 INTERGENIC REGION		UNCLASSIFIED	1001, 1004, 1006, 1009, 1010, 1017, 1022, 1024, 1034
7404	27823645 (6791, 6792)	Novel Protein sim. GBank gij1723669 sp P53235 YG22_YEAST - HYPOTHETICAL 71.3 KD PROTEIN IN SCM4- MUP1 INTERGENIC REGION		UNCLASSIFIED	1024
7405	5602652 (8819, 8820)	Novel Protein sim. GBank gij1723688 sp P53255 YG2M_YEAST - HYPOTHETICAL 58.2 KD PROTEIN IN DBF2- VAS1 INTERGENIC REGION		UNCLASSIFIED	1058
7406	79775783 (893, 894)	Novel Protein sim. GBank gij1723691 sp P53259 YG2Q_YEAST - HYPOTHETICAL 38.8 KD PROTEIN IN MIC1- SRB5 INTERGENIC REGION		UNCLASSIFIED	1008, 1017

7407	11084202 (6749, 6750)	Novel Protein sim. GBank gil1723693 sp P53261 YG2S_YEAST - HYPOTHETICAL 69.9 KD PROTEIN IN MIC1- SRB5 INTERGENIC REGION		UNCLASSIFIED	1024
7408	79829257 (9199, 9200)	Novel Protein sim. GBank gil1723697 sp P53265 YG2W_YEAST - HYPOTHETICAL 46.7 KD PROTEIN IN CLB6- SPT6 INTERGENIC REGION		UNCLASSIFIED	1025
7409	39548985 (18627, 18628)	Novel Protein sim. GBank gil1723697 sp P53265 YG2W_YEAST - HYPOTHETICAL 46.7 KD PROTEIN IN CLB6- SPT6 INTERGENIC REGION		UNCLASSIFIED	1003, 1006, 1008, 1038
7410	79951236 (13683, 13684)	Novel Protein sim. GBank gil1723722 sp P53290 YG3T_YEAST - HYPOTHETICAL 38.6 KD PROTEIN IN TIF4631- KRE11 INTERGENIC REGION		UNCLASSIFIED	1001
7411	57292347 (15071, 15072)	Novel Protein sim. GBank gil1723723 sp P53291 YG3U_YEAST - VERY HYPOTHETICAL 13.2 KD PROTEIN IN TIF4631- KRE11 INTERGENIC REGION		UNCLASSIFIED	1004, 1006, 1022, 1024, 1026, 1034, 1038
7412	19883491 (4115, 4116)	Novel Protein sim. GBank gil1723744 sp P50078 YG4P_YEAST - HYPOTHETICAL 69.6 KD PROTEIN IN MRPL9- PET54 INTERGENIC REGION		UNCLASSIFIED	1022
7413	79824860 (8845, 8846)	Novel Protein sim. GBank gil1723760 sp P53311 YG56_YEAST - HYPOTHETICAL 16.2 KD PROTEIN IN PFK1- TDS4 INTERGENIC REGION		UNCLASSIFIED	1003, 1025, 1044
7414	27849068 (17725, 17726)	Novel Protein sim. GBank gil1723800 sp P25338 YGB0_YEAST - HYPOTHETICAL 20.2 KD PROTEIN IN PRS2- LEU1 INTERGENIC REGION		UNCLASSIFIED	1022, 1034
7415	8489295 (11827, 11828)	Novel Protein sim. GBank gil1723843 sp P53168 YGG1_YEAST - HYPOTHETICAL 27.5 KD PROTEIN IN PYC1- UBC2 INTERGENIC REGION		UNCLASSIFIED	1024

7416	79569157 (11441, 11442)	Novel Protein sim. GBank gi 1723889 sp P40719 YGIY_ECOLI - PROBABLE SENSOR PROTEIN YGIY		UNCLASSIFIED	1008
7417	27955258 (13659, 13660)	Novel Protein sim. GBank gi 1723922 sp P53121 YGN9_YEAST - HYPOTHETICAL 90.8 KD PROTEIN IN MRP1- SEC27 INTERGENIC REGION		UNCLASSIFIED	1006, 1017, 1022, 1054
7418	10326965 (1325, 1326)	Novel Protein sim. GBank gi 1723968 sp P53076 YGX7_YEAST - HYPOTHETICAL 108.2 KD PROTEIN IN SAP4- OST5 INTERGENIC REGION		UNCLASSIFIED	1038
7419	80249073 (17413, 17414)	Novel Protein sim. GBank gi 1724031 sp P53633 YIPC_YEAST - YIP3 PROTEIN		UNCLASSIFIED	1003, 1006, 1026, 1039
7420	32122283 (243, 244)	Novel Protein sim. GBank gi 1729785 emb CAA70933 - (Y09798) function unknown [Pseudomonas fluorescens]		UNCLASSIFIED	1044
7421	10920589 (21007, 21008)	Novel Protein sim. GBank gi 1729852 sp Q02457 TBF1_YEAST - TBF1 PROTEIN (TTAGGG REPEAT-BINDING FACTOR 1) (TBF ALPHA)		UNCLASSIFIED	1024
7422	39564523 (1431, 1432)	Novel Protein sim. GBank gi 1730572 sp P52960 PIP2_YEAST - PEROXISOME PROLIFERATION TRANSCRIPTIONAL REGULATOR		UNCLASSIFIED	1006, 1009, 1023, 1025, 1034, 1044
7423	80217521 (14595, 14596)	Novel Protein sim. GBank gi 1730572 sp P52960 PIP2_YEAST - PEROXISOME PROLIFERATION TRANSCRIPTIONAL REGULATOR		UNCLASSIFIED	1004, 1006, 1008, 1009, 1016, 1022, 1034, 1038, 1044
7424	57292902 (1719, 1720)	Novel Protein sim. GBank gi 1730592 sp P49954 YLR85_YEAST - HYPOTHETICAL 32.5 KD PROTEIN YLR351C		UNCLASSIFIED	1006, 1010, 1022
7425	79865528 (2669, 2670)	Novel Protein sim. GBank gi 1730621 sp P53759 YMI0_YEAST - HYPOTHETICAL 48.1 KD PROTEIN IN TUB1- CPR3 INTERGENIC REGION		UNCLASSIFIED	1001, 1017, 1025, 1038

7433	79262053 (20007, 20008)	Novel Protein sim. GBank gil1730729 sp P53955 YNE7_YEAST - HYPOTHETICAL 74.8 KD PROTEIN IN AIG11.		UNCLASSIFIED	1008
7426	94321703 (12349, 12350)	Novel Protein sim. GBank gil1730634 sp P53845 YN03_YEAST - HYPOTHETICAL 35.5 KD PROTEIN IN PIK1- POL2 INTERGENIC REGION		UNCLASSIFIED	1001, 1003, 1004, 1006, 1008, 1017, 1022, 1024, 1028, 1031, 1034, 1038, 1044
7427	79264194 (13923, 13924)	Novel Protein sim. GBank gil1730634 sp P53845 YN03_YEAST - HYPOTHETICAL 35.5 KD PROTEIN IN PIK1- POL2 INTERGENIC REGION		UNCLASSIFIED	1003
7428	23290144 (9153, 9154)	Novel Protein sim. GBank gil1730646 sp P53833 POP3_YEAST - RNA PROCESSING PROTEIN POP3		UNCLASSIFIED	1017
7429	78527204 (18783, 18784)	Novel Protein sim. GBank gil1730665 sp P53721 YN89_YEAST - HYPOTHETICAL 25.3 KD PROTEIN IN TIM23- ARE2 INTERGENIC REGION		UNCLASSIFIED	1003
7430	80217805 (3531, 3532)	Novel Protein sim. GBank gil1730671 sp P53727 YN8F_YEAST - HYPOTHETICAL 35.4 KD PROTEIN IN SEC12- SSK2 INTERGENIC REGION		UNCLASSIFIED	1004, 1006, 1010, 1017, 1022, 1023, 1024, 1044
7431	88095468 (5983, 5984)	Novel Protein sim. GBank gil1730709 sp P53976 YNB8_YEAST - HYPOTHETICAL 69.6 KD PROTEIN IN HDA1- PUB1 INTERGENIC REGION		UNCLASSIFIED	1001, 1003, 1004, 1006, 1008, 1009, 1010, 1012, 1016, 1017, 1022, 1023, 1024, 1025, 1031, 1034, 1038, 1039, 1044, 1054
7432	78747510 (16813, 16814)	Novel Protein sim. GBank gil1730725 sp P53959 YNE1_YEAST -		UNCLASSIFIED	1026

7442	8022641 (22751, 22752)	Novel Protein sim. GBank gi 1731284 sp Q10815 YX25_MYCTU - PROBABLE INTEGRASE/RECOMBINASE CY274.25C		UNCLASSIFIED	1034
7443	17127322 (19371, 19372)	Novel Protein sim. GBank gi 173164 (J02719) - valyl-tRNA synthetase [Saccharomyces cerevisiae]		UNCLASSIFIED	1017
7444	66694404 (2407, 2408)	Novel Protein sim. GBank gi 1732455 dbj BAA09692 - (D63377) 2-hydroxypenta-2,4-dienoate hydratase [Pseudomonas fluorescens]		UNCLASSIFIED	1009
7445	21637972 (2711, 2712)	Novel Protein sim. GBank gi 1742118 dbj BAA148571 - (D90767) Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase). [Escherichia coli]		UNCLASSIFIED	1039
7446	8501105 (4333, 4334)	Novel Protein sim. GBank gi 1762939 (U66266) - ORF; able to induce HR-like lesions [Nicotiana tabacum]		UNCLASSIFIED	1004
7447	80061648 (21553, 21554)	Novel Protein sim. GBank gi 1770060 emb CAA9555.1 - (Z75208) hypothetical protein [Bacillus subtilis]		UNCLASSIFIED	1024
7448	66694969 (10387, 10388)	Novel Protein sim. GBank gi 1772622 (L39897) - HecB [Erwinia chrysanthemi]		UNCLASSIFIED	1009
7449	11102268 (21671, 21672)	Novel Protein sim. GBank gi 1787014 (AE000181) - putative transcriptional regulator [Escherichia coli]		UNCLASSIFIED	1006
7450	10194321 (20201, 20202)	Novel Protein sim. GBank gi 1787692 (AE000239) - orf, hypothetical protein [Escherichia coli]		UNCLASSIFIED	1003
7451	32164714 (22231, 22232)	Novel Protein sim. GBank gi 1787799 (AE000249) - orf, hypothetical protein [Escherichia coli]		UNCLASSIFIED	1023
7452	78459813 (3273, 3274)	Novel Protein sim. GBank gi 1788664 (AE000321) - putative peptidase [Escherichia coli]		UNCLASSIFIED	1026

7453	27830844 (1489, 1490)	Novel Protein sim. GBank gij1788881 (AE000339) - putative ATP synthase beta subunit [Escherichia coli]		UNCLASSIFIED	1022
7454	16502457 (8883, 8884)	Novel Protein sim. GBank gij1794286 (U76606) - isobutylamine N-hydroxylase [Streptomyces viridifaciens]		UNCLASSIFIED	1008
7455	70949006 (22773, 22774)	Novel Protein sim. GBank gij1817699[emb]CAB06573] - (Z84724) hypothetical protein Rv0433 [Mycobacterium tuberculosis]		UNCLASSIFIED	1029
7456	20622207 (17387, 17388)	Novel Protein sim. GBank gij1835114[emb]CAA71733] - (Y10744) homoserine O-acetyltransferase [Leptospira meyeri]		UNCLASSIFIED	1004, 1025, 1034, 1039
7457	33198842 (13471, 13472)	Novel Protein sim. GBank gij1835124[emb]CAA71005] - (Y09878) unnamed protein product [Mus musculus]		UNCLASSIFIED	1029
7458	79259307 (7561, 7562)	Novel Protein sim. GBank gij1835220[emb]CAA62445] - (X90950) Rga1p (Dbm1p) [Saccharomyces cerevisiae]		UNCLASSIFIED	1003, 1023
7459	54594425 (3679, 3680)	Novel Protein sim. GBank gij1838991[emb]CAB06635] - (Z85982) lysX [Mycobacterium tuberculosis]		UNCLASSIFIED	1029
7460	78459845 (7751, 7752)	Novel Protein sim. GBank gij1840087 (U83280) - 39 kDa antigen [Leishmania donovani]		UNCLASSIFIED	1026
7461	78374226 (12929, 12930)	Novel Protein sim. GBank gij1840087 (U83280) - 39 kDa antigen [Leishmania donovani]		UNCLASSIFIED	1003
7462	80421061 (12289, 12290)	Novel Protein sim. GBank gij1841968 (U67315) - unknown [Pseudomonas alcaligenes]		UNCLASSIFIED	1006, 1025
7463	18567497 (18539, 18540)	Novel Protein sim. GBank gij1850111[emb]CAB06678] - (Z86089) hypothetical protein Rv0266c [Mycobacterium tuberculosis]		UNCLASSIFIED	1001
7464	28390204 (4475, 4476)	Novel Protein sim. GBank gij1864013[dbj]BAA13520] - (D87967) SHPS-1 [Mus musculus]		UNCLASSIFIED	1044

7465	80244146 (14829, 14830)	Novel Protein sim. GBank gil1870003[emb CAB06854] - (Z92539) hypothetical protein Rv1025 [Mycobacterium tuberculosis]		UNCLASSIFIED	1006, 1022, 1024
7466	20708208 (1609, 1610)	Novel Protein sim. GBank gil1870010[emb CAB06861] - (Z92539) glmU [Mycobacterium tuberculosis]		UNCLASSIFIED	1008
7467	20473946 (8759, 8760)	Novel Protein sim. GBank gil1870011[emb CAB06862] - (Z92539) prsA [Mycobacterium tuberculosis]		UNCLASSIFIED	1010
7468	30788874 (13143, 13144)	Novel Protein sim. GBank gil1877301[emb CAB07144] - (Z92774) hypothetical protein Rv3570c [Mycobacterium tuberculosis]		UNCLASSIFIED	1016, 1026
7469	25263673 (11919, 11920)	Novel Protein sim. GBank gil1881254[dbj BAA19281] - (AB001488) SIMILAR TO C4-DICARBOXYLATE-BINDING PERIPLASMIC PROTEIN OF RHODOBACTER CAPSULATUS, [Bacillus subtilis]		UNCLASSIFIED	1026
7470	94666728 (5995, 5996)	Novel Protein sim. GBank gil1906369[emb CAA72726] - (Y11998) hypothetical protein [Pseudomonas fluorescens]		UNCLASSIFIED	1006
7471	16499982 (17881, 17882)	Novel Protein sim. GBank gil1916229 (U83303) - line-1 reverse transcriptase [Homo sapiens]		UNCLASSIFIED	1030
7472	79488452 (19143, 19144)	Novel Protein sim. GBank gil1929089[emb CAB07817] - (Z93777) hypothetical protein Rv1215c [Mycobacterium tuberculosis]		UNCLASSIFIED	1027
7473	78078007 (20613, 20614)	Novel Protein sim. GBank gil1934732 (U96128) - UDP-galactopyranose mutase [Mycobacterium tuberculosis]		UNCLASSIFIED	1029
7474	36755672 (1729, 1730)	Novel Protein sim. GBank gil1933330 (U82303) - unknown [Homo sapiens]		UNCLASSIFIED	1034
7475	79831074 (20301, 20302)	Novel Protein sim. GBank gil1942489[pdb 1REQ B - Chain B, Methylmalonyl-CoA Mutase]		UNCLASSIFIED	1023

7476	81932612 (12825, 12826)	Novel Protein sim. GBank gi 1844391 db BAA19565 - (D86413) Ern4p [Saccharomyces cerevisiae]		UNCLASSIFIED	1000, 1001, 1003, 1004, 1006, 1008, 1009, 1010, 1012, 1016, 1017, 1022, 1023, 1024, 1028, 1027, 1031, 1034, 1038, 1039, 1044, 1054
7477	65657188 (4513, 4514)	Novel Protein sim. GBank gi 198646 (M29324) - ORF2; 5' end undetermined. [Mus musculus]		UNCLASSIFIED	1054
7478	11084375 (6427, 6428)	Novel Protein sim. GBank gi 2058299 emb CAA66953 - (X98309) ARI protein [Drosophila melanogaster]		UNCLASSIFIED	1010
7479	57292546 (20891, 20892)	Novel Protein sim. GBank gi 2062680 (U88964) - HEM45 [Homo sapiens]		UNCLASSIFIED	1004, 1016
7480	78503017 (19097, 19098)	Novel Protein sim. GBank gi 2065209 emb CAA73250 - (Y12713) Gag polypeptide [Mus musculus]		UNCLASSIFIED	1026
7481	71122286 (10953, 10954)	Novel Protein sim. GBank gi 2065210 emb CAA73251 - (Y12713) Pro-Pol-dUTPase polypeptide [Mus musculus]		UNCLASSIFIED	1016
7482	80104933 (11695, 11696)	Novel Protein sim. GBank gi 2065210 emb CAA73251 - (Y12713) Pro-Pol-dUTPase polypeptide [Mus musculus]		UNCLASSIFIED	1010
7483	65641894 (12781, 12782)	Novel Protein sim. GBank gi 2065210 emb CAA73251 - (Y12713) Pro-Pol-dUTPase polypeptide [Mus musculus]		UNCLASSIFIED	1016
7484	79558374 (17197, 17198)	Novel Protein sim. GBank gi 2065210 emb CAA73251 - (Y12713) Pro-Pol-dUTPase polypeptide [Mus musculus]		UNCLASSIFIED	1038
7485	46887745 (22711, 22712)	Novel Protein sim. GBank gi 2065210 emb CAA73251 - (Y12713) Pro-Pol-dUTPase polypeptide [Mus musculus]		UNCLASSIFIED	1037

7486	36732609 (13277, 13278)	Novel Protein sim. GBank gjl2072948 (U93563) - putative p150 [Homo sapiens]	UNCLASSIFIED	1023
7487	86686154 (12379, 12380)	Novel Protein sim. GBank gjl2072951 (U93564) - putative p150 [Homo sapiens]	UNCLASSIFIED	1018
7488	65886038 (17937, 17938)	Novel Protein sim. GBank gjl2072951 (U93564) - putative p150 [Homo sapiens]	UNCLASSIFIED	1029
7489	66645483 (17415, 17416)	Novel Protein sim. GBank gjl2072955 (U93566) - p40 [Homo sapiens]	UNCLASSIFIED	1041
7490	37014367 (1127, 1128)	Novel Protein sim. GBank gjl2072967 (U93570) - putative p150 [Homo sapiens]	UNCLASSIFIED	1029
7491	78677077 (2303, 2304)	Novel Protein sim. GBank gjl2072967 (U93570) - putative p150 [Homo sapiens]	UNCLASSIFIED	1026
7492	13523238 (16401, 16402)	Novel Protein sim. GBank gjl2072967 (U93570) - putative p150 [Homo sapiens]	UNCLASSIFIED	1004
7493	30176122 (20253, 20254)	Novel Protein sim. GBank gjl2072972 (U93572) - putative p150 [Homo sapiens]	UNCLASSIFIED	1029
7494	19882024 (1599, 1600)	Novel Protein sim. GBank gjl2076670[emb]CAB08387] - (Z95150) hypothetical protein Rv3095 [Mycobacterium tuberculosis]	UNCLASSIFIED	1034
7495	85806873 (18477, 18478)	Novel Protein sim. GBank gjl2078009[emb]CAB08456] - (Z95207) hypothetical protein Rv2850c [Mycobacterium tuberculosis]	UNCLASSIFIED	1054
7496	95287796 (14669, 14670)	Novel Protein sim. GBank gjl2078024[emb]CAB08477] - (Z95208) hypothetical protein Rv2375 [Mycobacterium tuberculosis]	UNCLASSIFIED	1006, 1008, 1009, 1012, 1024
7497	80478399 (3825, 3826)	Novel Protein sim. GBank gjl2078483 (U43200) - antifreeze glycopeptide AFGP polypeptide precursor [Boreogadus saida]	UNCLASSIFIED	1012
7498	80048270 (16845, 16846)	Novel Protein sim. GBank gjl2078483 (U43200) - antifreeze glycopeptide AFGP polypeptide precursor [Boreogadus saida]	UNCLASSIFIED	1004, 1027
7499	80468619 (20951, 20952)	Novel Protein sim. GBank gjl2094844[emb]CAB08571] - (Z95324) fba [Mycobacterium tuberculosis]	UNCLASSIFIED	1012, 1038

7500	19880484 (14413, 14414)	Novel Protein sim. GBank gi 2104338 emb CAB08653 - (Z95388) hypothetical protein Rv2140c [Mycobacterium tuberculosis]		UNCLASSIFIED	1034
7501	37801575 (5187, 5188)	Novel Protein sim. GBank gi 2104375 emb CAB08718 - (Z95390) hypothetical protein Rv3452 [Mycobacterium tuberculosis]		UNCLASSIFIED	1012
7502	78240045 (5217, 5218)	Novel Protein sim. GBank gi 2104600 emb CAB08809 - (Z95398) unknown [Mycobacterium leprae]		UNCLASSIFIED	1026
7503	35062334 (18629, 18630)	Novel Protein sim. GBank gi 2113990 emb CAB08995 - (Z95558) hypothetical protein Rv0528 [Mycobacterium tuberculosis]		UNCLASSIFIED	1024
7504	78481280 (18653, 18654)	Novel Protein sim. GBank gi 2114473 (U96963) - p140mDia [Mus musculus]		UNCLASSIFIED	1026
7505	65680609 (2035, 2036)	Novel Protein sim. GBank gi 2117310 emb CAB09116.1 - (Z95620) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	1030, 1041
7506	46571634 (7333, 7334)	Novel Protein sim. GBank gi 2117310 emb CAB09116.1 - (Z95620) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	1029
7507	78905075 (8509, 8510)	Novel Protein sim. GBank gi 2117310 emb CAB09116.1 - (Z95620) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	1003
7508	78300286 (2877, 2878)	Novel Protein sim. GBank gi 2119898 pir S49550 - M-like protein emmL9 - Streptococcus pyogenes (strain 71-683)		UNCLASSIFIED	1030, 1054
7509	80040488 (19007, 19008)	Novel Protein sim. GBank gi 2120070 pir S69973 - TyB protein - yeast (Saccharomyces cerevisiae) retrotransposon Ty2.N		UNCLASSIFIED	1004, 1006, 1058

7521	57530381 (5625, 5626)	Novel Protein sim. GBank gj2131367 pir S67786 - hypothetical protein YDL223c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003, 1006, 1012, 1017, 1022, 1024, 1026, 1034
7522	65481450 (59, 60)	Novel Protein sim. GBank gj2131404 pir S70126 - hypothetical protein YDR266c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1049
7523	80044676 (12949, 12950)	Novel Protein sim. GBank gj2131443 pir S61155 - hypothetical protein YDR359c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006
7524	29449628 (45, 46)	Novel Protein sim. GBank gj2131446 pir S61157 - hypothetical protein YDR362c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1026
7525	78747500 (14261, 14262)	Novel Protein sim. GBank gj2131449 pir S69746 - hypothetical protein YDR366c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003, 1026
7526	80205726 (9709, 9710)	Novel Protein sim. GBank gj2131466 pir S69681 - hypothetical protein YDR398w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006, 1008, 1017, 1022, 1024, 1025, 1026, 1034, 1038
7527	27835905 (7661, 7662)	Novel Protein sim. GBank gj2131501 pir S69731 - hypothetical protein YDR452w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003, 1006, 1024, 1034
7528	27838166 (4411, 4412)	Novel Protein sim. GBank gj2131505 pir S69625 - hypothetical protein YDR457w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1024
7529	8359865 (15541, 15542)	Novel Protein sim. GBank gj2131510 pir S69634 - hypothetical protein YDR466w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1024
7530	27963931 (10999, 11000)	Novel Protein sim. GBank gj2131529 pir S69660 - hypothetical protein YDR493w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003, 1006, 1034

7531	804311196 (6761, 6762)	Novel Protein sim. GBank gi2131541 pir S69574 - hypothetical protein YDR517w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1001, 1003, 1006, 1008, 1012, 1016, 1017, 1022, 1023, 1024, 1026, 1031, 1034, 1038, 1039, 1044
7532	80502906 (4781, 4782)	Novel Protein sim. GBank gi2131542 pir S69577 - hypothetical protein YDR520c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1004, 1006, 1010, 1012, 1017, 1022, 1024, 1034
7533	80478058 (17271, 17272)	Novel Protein sim. GBank gi2131542 pir S69577 - hypothetical protein YDR520c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1004, 1006, 1008, 1009, 1012, 1022, 1023, 1024, 1026, 1030, 1034, 1039
7534	80019606 (9793, 9794)	Novel Protein sim. GBank gi2131545 pir S69581 - hypothetical protein YDR525w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006, 1025, 1027, 1034
7535	79625779 (441, 442)	Novel Protein sim. GBank gi2131548 pir S69583 - hypothetical protein YDR528w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006, 1017
7536	27842289 (3801, 3802)	Novel Protein sim. GBank gi2131776 pir S64933 - hypothetical protein YLR099c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1022
7537	13519757 (2235, 2236)	Novel Protein sim. GBank gi2131778 pir S64944 - hypothetical protein YLR107w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1024
7538	95011183 (21845, 21846)	Novel Protein sim. GBank gi2131791 pir S65003 - hypothetical protein YLR154c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1001, 1003, 1004, 1010, 1012, 1022, 1023, 1024, 1026

7539	57294978 (10369, 10370)	Novel Protein sim. GBank gjl2131820 pir S69871 - hypothetical protein YML012c-a - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1004, 1006, 1008, 1022, 1024, 1031, 1034, 1038
7540	80226467 (6279, 6280)	Novel Protein sim. GBank gjl2131997 pir S66717 - hypothetical protein YOL034w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1004, 1008, 1009, 1017, 1022, 1024, 1026, 1034, 1039
7541	79318993 (2467, 2468)	Novel Protein sim. GBank gjl2132008 pir S66765 - hypothetical protein YOL072w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1034
7542	78677090 (5093, 5094)	Novel Protein sim. GBank gjl2132036 pir S66923 - hypothetical protein YOR049c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003, 1026
7543	3696917 (12291, 12292)	Novel Protein sim. GBank gjl2132046 pir S66953 - hypothetical protein YOR070c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1012
7544	30404307 (19565, 19566)	Novel Protein sim. GBank gjl2132048 pir S66959 - hypothetical protein YOR076c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1008
7545	30404479 (20045, 20046)	Novel Protein sim. GBank gjl2132048 pir S66959 - hypothetical protein YOR076c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1008
7546	85513670 (4671, 4672)	Novel Protein sim. GBank gjl2132051 pir S61644 - hypothetical protein YOR083w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1001, 1003, 1006, 1010, 1017, 1022, 1023, 1034, 1039, 1044, 1049
7547	80240865 (8373, 8374)	Novel Protein sim. GBank gjl2132058 pir S61668 - hypothetical protein YOR110w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1001, 1003, 1004, 1006, 1008, 1009, 1010, 1016, 1017, 1022, 1023, 1024, 1026, 1034, 1039, 1044, 1054

7548	78742231 (11281, 11282)	Novel Protein sim. GBank gij2132066 pir S60988 - hypothetical protein YOR134w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1022
7549	17743829 (13223, 13224)	Novel Protein sim. GBank gij2132067 pir S61698 - hypothetical protein YOR144c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1044
7550	27844553 (5643, 5644)	Novel Protein sim. GBank gij2132087 pir S60947 - hypothetical protein YOR220w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006
7551	30266586 (11755, 11756)	Novel Protein sim. GBank gij2132103 pir S67155 - hypothetical protein YOR258w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1024
7552	80216691 (19881, 19882)	Novel Protein sim. GBank gij2132113 pir S67186 - hypothetical protein YOR284w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003, 1004, 1006, 1008, 1009, 1010, 1022, 1024, 1026, 1027, 1030, 1034, 1038, 1039, 1044
7553	80428123 (7417, 7418)	Novel Protein sim. GBank gij2132147 pir S59679 - hypothetical protein YPL014w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003, 1004, 1006, 1024, 1025, 1034
7554	20262048 (21789, 21790)	Novel Protein sim. GBank gij2132153 pir S63458 - hypothetical protein YPL024w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1022
7555	5469539 (10377, 10378)	Novel Protein sim. GBank gij2132186 pir S61970 - hypothetical protein YPL096w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1058
7556	86380059 (9757, 9758)	Novel Protein sim. GBank gij2132189 pir S61960 - hypothetical protein YPL107w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1053
7557	65481779 (3725, 3726)	Novel Protein sim. GBank gij2132190 pir S61959 - hypothetical protein YPL108w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1049
7558	78742065 (18459, 18460)	Novel Protein sim. GBank gij2132232 pir S65227 - hypothetical protein YPL208w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1008, 1009, 1022, 1039

7559	79111339 (12103, 12104)	Novel Protein sim. GBank gi 2132241 pir S61701 - hypothetical protein YPL233w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003, 1039
7560	79579586 (2157, 2158)	Novel Protein sim. GBank gi 2132244 pir S61023 - hypothetical protein YPL242c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1004, 1022
7561	80219478 (6659, 6660)	Novel Protein sim. GBank gi 2132265 pir S70044 - hypothetical protein YPR077c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1004, 1029, 1034, 1039
7562	80479572 (19531, 19532)	Novel Protein sim. GBank gi 2132273 pir S69074 - hypothetical protein YPR090w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1001, 1003, 1004, 1006, 1008, 1009, 1010, 1012, 1016, 1017, 1022, 1023, 1024, 1026, 1027, 1034, 1039, 1044
7563	52557997 (21467, 21468)	Novel Protein sim. GBank gi 2132273 pir S69074 - hypothetical protein YPR090w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1054
7564	80219161 (13661, 13662)	Novel Protein sim. GBank gi 2132285 pir S59773 - hypothetical protein YPR108w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003, 1004, 1006, 1010, 1017, 1022, 1023, 1025, 1031
7565	80227275 (1597, 1598)	Novel Protein sim. GBank gi 2132299 pir S69029 - hypothetical protein YPR140w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1022, 1034
7566	10251496 (10445, 10446)	Novel Protein sim. GBank gi 2132313 pir S59830 - hypothetical protein YPR172w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1038
7567	79256284 (2865, 2866)	Novel Protein sim. GBank gi 2132353 pir S42160 - MSS51 protein - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003, 1022

7568	29680966 (19215, 19216)	Novel Protein sim. GBank gij2132444 pir S67694 - probable membrane protein YDL146w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1009
7569	27824338 (13079, 13080)	Novel Protein sim. GBank gij2132460 pir S67781 - probable membrane protein YDL218w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1024
7570	11304673 (22139, 22140)	Novel Protein sim. GBank gij2132462 pir S67794 - probable membrane protein YDL231c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1034
7571	78791459 (4743, 4744)	Novel Protein sim. GBank gij2132487 pir S70134 - probable membrane protein YDR278c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1022
7572	28397253 (11401, 11402)	Novel Protein sim. GBank gij2132491 pir S70114 - probable membrane protein YDR284c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1039
7573	94672659 (1619, 1620)	Novel Protein sim. GBank gij2132502 pir S59792 - probable membrane protein YDR326c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1022
7574	95295893 (6197, 6198)	Novel Protein sim. GBank gij2132508 pir S61149 - probable membrane protein YDR352w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1022, 1025
7575	80205918 (2025, 2026)	Novel Protein sim. GBank gij2132649 pir S64771 - probable membrane protein YLL023c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1008, 1022, 1024, 1025, 1026, 1034, 1038
7576	80216897 (21771, 21772)	Novel Protein sim. GBank gij2132649 pir S64771 - probable membrane protein YLL023c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003, 1006, 1008, 1022, 1024, 1034, 1039, 1044

7577	37010090 (6351, 6352)	Novel Protein sim. GBank gi 2132661 pir S64842 - probable membrane protein YLR020c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1029
7578	94239989 (21231, 21232)	Novel Protein sim. GBank gi 2132663 pir S64851 - probable membrane protein YLR024c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1017
7579	28477139 (17711, 17712)	Novel Protein sim. GBank gi 2132667 pir S64869 - probable membrane protein YLR042c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1008
7580	80215889 (10567, 10568)	Novel Protein sim. GBank gi 2132679 pir S64916 - probable membrane protein YLR084c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1004, 1006, 1010, 1022, 1024, 1034
7581	30645909 (11855, 11856)	Novel Protein sim. GBank gi 2132679 pir S64916 - probable membrane protein YLR084c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1008
7582	27838227 (17267, 17268)	Novel Protein sim. GBank gi 2132680 pir S64921 - probable membrane protein YLR087c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006
7583	23288283 (4893, 4894)	Novel Protein sim. GBank gi 2132817 pir S61981 - probable membrane protein YOL003c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003
7584	11594169 (18327, 18328)	Novel Protein sim. GBank gi 2132839 pir S66766 - probable membrane protein YOL073c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1034
7585	78385738 (13647, 13648)	Novel Protein sim. GBank gi 2132846 pir S66816 - probable membrane protein YOL119c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1026

7586	82056110 (10809, 10810)	Novel Protein sim. GBank gj2132852 pir S66835 - probable membrane protein YOL138c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006, 1010, 1016, 1022, 1024
7587	79861380 (15847, 15848)	Novel Protein sim. GBank gj2132852 pir S66835 - probable membrane protein YOL138c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1025
7588	80216050 (14435, 14436)	Novel Protein sim. GBank gj2132853 pir S60390 - probable membrane protein YOL146w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006, 1024, 1025, 1026, 1039
7589	95295784 (8587, 8588)	Novel Protein sim. GBank gj2132878 pir S61645 - probable membrane protein YOR084w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1001, 1006, 1008, 1017, 1022, 1023, 1038
7590	27974805 (15461, 15462)	Novel Protein sim. GBank gj2132880 pir S66972 - probable membrane protein YOR087w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006
7591	8371339 (10795, 10796)	Novel Protein sim. GBank gj2132882 pir S61654 - probable membrane protein YOR093c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1004
7592	94655445 (4283, 4284)	Novel Protein sim. GBank gj2132889 pir S61667 - probable membrane protein YOR109w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1001, 1003, 1004, 1006, 1008, 1010, 1012, 1016, 1017, 1022, 1023, 1024, 1034, 1038, 1039
7593	80217723 (17475, 17476)	Novel Protein sim. GBank gj2132900 pir S67042 - probable membrane protein YOR154w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006, 1008, 1022, 1024

7594	20687033 (6765, 6766)	Novel Protein sim. GBank gi 2132901 pir S67049 - probable membrane protein YOR161c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1024
7595	80232871 (10687, 10688)	Novel Protein sim. GBank gi 2132902 pir S67050 - probable membrane protein YOR162c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1004, 1008, 1009, 1022, 1044
7596	29346134 (9567, 9568)	Novel Protein sim. GBank gi 2132903 pir S67053 - probable membrane protein YOR165w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1022
7597	11302078 (18577, 18578)	Novel Protein sim. GBank gi 2132903 pir S67053 - probable membrane protein YOR165w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1024
7598	20728259 (1975, 1976)	Novel Protein sim. GBank gi 2132917 pir S60941 - probable membrane protein YOR214c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006
7599	39547842 (2179, 2180)	Novel Protein sim. GBank gi 2132942 pir S67210 - probable membrane protein YOR306c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006, 1010, 1022, 1024, 1031, 1034
7600	78891211 (5569, 5570)	Novel Protein sim. GBank gi 2132947 pir S58333 - probable membrane protein YOR322c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003
7601	78780706 (11765, 11766)	Novel Protein sim. GBank gi 2132947 pir S58333 - probable membrane protein YOR322c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1009
7602	17892403 (22047, 22048)	Novel Protein sim. GBank gi 2132947 pir S58333 - probable membrane protein YOR322c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1039

7603	80216496 (21085, 21086)	Novel Protein sim. GBank gjl2132965 pir S67303 - probable membrane protein YOR391c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1004, 1006, 1008, 1010, 1017, 1022, 1024, 1031, 1034, 1038
7604	37810436 (1649, 1650)	Novel Protein sim. GBank gjl2132974 pir S60930 - probable membrane protein YPL060w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1058
7605	30643448 (13617, 13618)	Novel Protein sim. GBank gjl2132975 pir S61116 - probable membrane protein YPL070w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1022
7606	80221176 (11241, 11242)	Novel Protein sim. GBank gjl2132983 pir S62009 - probable membrane protein YPL112c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006, 1008, 1009, 1010, 1017, 1022, 1024, 1025
7607	17088016 (20927, 20928)	Novel Protein sim. GBank gjl2133004 pir S65240 - probable membrane protein YPL221w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1023
7608	65466546 (22787, 22788)	Novel Protein sim. GBank gjl2133004 pir S65240 - probable membrane protein YPL221w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1010
7609	80227049 (22957, 22958)	Novel Protein sim. GBank gjl2133006 pir S61026 - probable membrane protein YPL238c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1004, 1006, 1008, 1017, 1024, 1034
7610	78516982 (16291, 16292)	Novel Protein sim. GBank gjl2133016 pir S65310 - probable membrane protein YPL277c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1008
7611	25241287 (17817, 17818)	Novel Protein sim. GBank gjl2133023 pir S69075 - probable membrane protein YPR091c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1009

7612	16399007 (5307, 5308)	Novel Protein sim. GBank gi 2133025 pir S59770 - probable membrane protein YPR105c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1017
7613	98602917 (4357, 4358)	Novel Protein sim. GBank gi 2133031 pir S59028 - probable membrane protein YPR139c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1001, 1004, 1006, 1010, 1012, 1022, 1023, 1025, 1054
7614	79818070 (11643, 11644)	Novel Protein sim. GBank gi 2133039 pir S59841 - probable membrane protein YPR184w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006
7615	28471403 (15925, 15926)	Novel Protein sim. GBank gi 2133039 pir S59841 - probable membrane protein YPR184w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1026
7616	78769950 (18637, 18638)	Novel Protein sim. GBank gi 2133082 pir S67314 - regulatory protein MSR1 - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1026
7617	27803028 (21833, 21834)	Novel Protein sim. GBank gi 2133082 pir S67314 - regulatory protein MSR1 - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1003, 1004, 1024, 1034
7618	20726205 (8205, 8206)	Novel Protein sim. GBank gi 2133091 pir S61716 - ribose-phosphate pyrophosphokinase PRPS3 homolog YOL061w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	1006
7619	10170101 (13213, 13214)	Novel Protein sim. GBank gi 2137043 pir 46880 - unknown protein - rabbit (fragment)		UNCLASSIFIED	1025
7620	94126265 (297, 298)	Novel Protein sim. GBank gi 2137756 pir 48746 - semaphorin C - mouse (fragment)		UNCLASSIFIED	1053
7621	35108236 (22163, 22164)	Novel Protein sim. GBank gi 2143878 pir 55615 - nitric-oxide synthase (EC 1.14.13.39) - rat		UNCLASSIFIED	1050

7622	78763064 (17237, 17238)	Novel Protein sim. GBank gi 2144206 pir S63864 - hypothetical protein 211 - Allomyces macrogynus mitochondrion	UNCLASSIFIED	1008, 1039
7623	11102552 (5743, 5744)	Novel Protein sim. GBank gi 2145653 pir S72762 - B1496_C2_194 protein - Mycobacterium leprae	UNCLASSIFIED	1006
7624	78785069 (537, 538)	Novel Protein sim. GBank gi 2146836 pir S74280 - hypothetical protein YCL054w - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	1008, 1009, 1022
7625	27981118 (15161, 15162)	Novel Protein sim. GBank gi 215574 (M64097) - E16 [Bacteriophage mu]	UNCLASSIFIED	1006
7626	79480752 (3833, 3834)	Novel Protein sim. GBank gi 2183285 (AF002860) - tuftelin [Mus musculus]	UNCLASSIFIED	1022, 1055
7627	79967999 (1171, 1172)	Novel Protein sim. GBank gi 2193870 dbj BAA20419 - (D84391) reverse transcriptase [Mus musculus]	UNCLASSIFIED	1034
7628	87455696 (8893, 8894)	Novel Protein sim. GBank gi 2193870 dbj BAA20419 - (D84391) reverse transcriptase [Mus musculus]	UNCLASSIFIED	1018
7629	65445062 (22553, 22554)	Novel Protein sim. GBank gi 2193870 dbj BAA20419 - (D84391) reverse transcriptase [Mus musculus]	UNCLASSIFIED	1038
7630	78047124 (22063, 22064)	Novel Protein sim. GBank gi 2196910 (U83169) - polythreonine protein [Cryptosporidium parvum]	UNCLASSIFIED	1054
7631	29020343 (19237, 19238)	Novel Protein sim. GBank gi 2213429 emb CAA63344 - (X92653) unknown product [Drosophila melanogaster]	UNCLASSIFIED	1017
7632	79425557 (4181, 4182)	Novel Protein sim. GBank gi 2224685 dbj BAA20827 - (AB002370) KIAA0372 [Homo sapiens]	UNCLASSIFIED	1038
7633	46571958 (15143, 15144)	Novel Protein sim. GBank gi 2224829 emb CAB10017 - (Z97188) hypothetical protein Rv3816c [Mycobacterium tuberculosis]	UNCLASSIFIED	1029

7634	8176133 (3977, 3978)	Novel Protein sim. GBank gil2224832[emb]CAB10018] - (Z97188) hypothetical protein Rv3813c [Mycobacterium tuberculosis]		UNCLASSIFIED	1022
7635	78980140 (3431, 3432)	Novel Protein sim. GBank gil2226004 (U49973) - ORF1; MER37; putative transposase similar to pogo element [Homo sapiens]		UNCLASSIFIED	1008
7636	65506326 (8355, 8356)	Novel Protein sim. GBank gil2226004 (U49973) - ORF1; MER37; putative transposase similar to pogo element [Homo sapiens]		UNCLASSIFIED	1016
7637	78717291 (13389, 13390)	Novel Protein sim. GBank gil2226004 (U49973) - ORF1; MER37; putative transposase similar to pogo element [Homo sapiens]		UNCLASSIFIED	1025
7638	30393743 (18127, 18128)	Novel Protein sim. GBank gil2226004 (U49973) - ORF1; MER37; putative transposase similar to pogo element [Homo sapiens]		UNCLASSIFIED	1054
7639	33189257 (6993, 6994)	Novel Protein sim. GBank gil2226005 (U49973) - ORF2: function unknown [Homo sapiens]		UNCLASSIFIED	1026
7640	55489578 (16875, 16876)	Novel Protein sim. GBank gil2226005 (U49973) - ORF2: function unknown [Homo sapiens]		UNCLASSIFIED	1026
7641	94641276 (2965, 2966)	Novel Protein sim. GBank gil2239236[emb]CAB10154] - (Z97211) probable involvement in ergosterol synthesis [Schizosaccharomyces pombe]		UNCLASSIFIED	1034
7642	7542334 (7253, 7254)	Novel Protein sim. GBank gil2244807[emb]CAB10230.1] - (Z97336) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	1058
7643	30161837 (3019, 3020)	Novel Protein sim. GBank gil2244854[emb]CAB10276.1] - (Z97337) hypothetical [Arabidopsis thaliana]		UNCLASSIFIED	1016
7644	11291903 (14785, 14786)	Novel Protein sim. GBank gil2252812[gb]AAB62820.1] - (AF004731) Stp22p [Saccharomyces cerevisiae]		UNCLASSIFIED	1024
7645	78740549 (7517, 7518)	Novel Protein sim. GBank gil2253585[gb]AAB63256.1] - (U69172) unknown [Mus musculus]		UNCLASSIFIED	1039

7646	79574930 (9543, 9544)	Novel Protein sim. GBank gi 2257708 (U73041) - transposase-like protein [Thiobacillus ferrooxidans]	UNCLASSIFIED	1031
7647	10141524 (3623, 3624)	Novel Protein sim. GBank gi 2271391 (AF009352) - osmoprotectant binding protein precursor [Bacillus subtilis]	UNCLASSIFIED	1025
7648	79552136 (8551, 8552)	Novel Protein sim. GBank gi 2276407 (L77976) - homoserimidine synthase [Blastochloris viridis]	UNCLASSIFIED	1039
7649	13763445 (2925, 2926)	Novel Protein sim. GBank gi 2280480 (dbj BAA21572) - (AB002344) KIAA0346 [Homo sapiens]	UNCLASSIFIED	1016
7650	86473972 (19637, 19638)	Novel Protein sim. GBank gi 2291142 (AF016417) - No definition line found [Caenorhabditis elegans]	UNCLASSIFIED	1054
7651	11291481 (17135, 17136)	Novel Protein sim. GBank gi 2292957 (emb CAB10899) - (Z98209) hypothetical protein Rv2723 [Mycobacterium tuberculosis]	UNCLASSIFIED	1010
7652	30371494 (18453, 18454)	Novel Protein sim. GBank gi 2292986 (emb CAA04133) - (AJ000496) cyclic nucleotide-gated channel beta subunit [Rattus norvegicus]	UNCLASSIFIED	1016
7653	20622189 (15233, 15234)	Novel Protein sim. GBank gi 2293257 (AF008220) - YtnM [Bacillus subtilis]	UNCLASSIFIED	1004
7654	14206236 (9761, 9762)	Novel Protein sim. GBank gi 2313487 (gb AAD07451.1) - (AE000555) zinc-metallo protease (YJR117W) [Helicobacter pylori 26695]	UNCLASSIFIED	1053
7655	14219143 (19543, 19544)	Novel Protein sim. GBank gi 2313638 (gb AAD07591.1) - (AE000566) cag pathogenicity island protein (cag5) [Helicobacter pylori 26695]	UNCLASSIFIED	1034
7656	14207029 (20955, 20956)	Novel Protein sim. GBank gi 2313798 (gb AAD07737.1) - (AE000580) H. pylori predicted coding region HP0669 [Helicobacter pylori 26695]	UNCLASSIFIED	1034

7657	20267403 (19431, 19432)	Novel Protein sim. GBank gil2313817 gb AAD07745.1 - (AE000582) conserved hypothetical integral membrane protein [Helicobacter pylori 26695]		UNCLASSIFIED	1010
7658	13883812 (12061, 12062)	Novel Protein sim. GBank gil2313940 gb AAD07858.1 - (AE000592) H. pylori predicted coding region HP0803 [Helicobacter pylori 26695]		UNCLASSIFIED	1053
7659	39523975 (15849, 15850)	Novel Protein sim. GBank gil2313984 gb AAD07898.1 - (AE000596) type I restriction enzyme M protein (hsdM) [Helicobacter pylori 26695]		UNCLASSIFIED	1004
7660	80209487 (10329, 10330)	Novel Protein sim. GBank gil2314013 gb AAD07926.1 - (AE000597) H. pylori predicted coding region HP0874 [Helicobacter pylori 26695]		UNCLASSIFIED	1034
7661	80209530 (20299, 20300)	Novel Protein sim. GBank gil2314144 gb AAD08046.1 - (AE000608) H. pylori predicted coding region HP0996 [Helicobacter pylori 26695]		UNCLASSIFIED	1034
7662	57288608 (4083, 4084)	Novel Protein sim. GBank gil2314247 gb AAD08141.1 - (AE000616) conserved hypothetical secreted protein [Helicobacter pylori 26695]		UNCLASSIFIED	1053
7663	20287152 (17523, 17524)	Novel Protein sim. GBank gil2314381 gb AAD08264.1 - (AE000627) D- lactate dehydrogenase (dld) [Helicobacter pylori 26695]		UNCLASSIFIED	1034
7664	13886351 (5621, 5622)	Novel Protein sim. GBank gil2314680 gb AAD08542.1 - (AE000648) glutamate permease (glis) [Helicobacter pylori 26695]		UNCLASSIFIED	1053
7665	20608459 (8711, 8712)	Novel Protein sim. GBank gil2326734 emb CAB10948 - (Z98288) hypothetical protein Rv1691 [Mycobacterium tuberculosis]		UNCLASSIFIED	1004

7666	77474079 (287, 288)	Novel Protein sim. GBank gi 2340009 emb CAB11359 - (Z98862) YlbM protein [Bacillus subtilis]		UNCLASSIFIED	1023, 1026
7667	24129321 (21639, 21640)	Novel Protein sim. GBank gi 2340850 emb CAA74067 - (Y13732) urease accessory protein [Ralstonia eutropha]		UNCLASSIFIED	1003
7668	65706325 (7393, 7394)	Novel Protein sim. GBank gi 2341020 gb AAC35295 - (AC002483) putative product from mRNA sequence CG003 from BRCA2 region; match to U50534 (NID:g1685103) [Homo sapiens]		UNCLASSIFIED	1001, 1038
7669	25233410 (11813, 11814)	Novel Protein sim. GBank gi 2341020 gb AAC35295 - (AC002483) putative product from mRNA sequence CG003 from BRCA2 region; match to U50534 (NID:g1685103) [Homo sapiens]		UNCLASSIFIED	1017
7670	28359669 (18123, 18124)	Novel Protein sim. GBank gi 2342526 emb CAA74694 - (Y14314) IgE autoantigen [Homo sapiens]		UNCLASSIFIED	1025
7671	47652669 (25, 26)	Novel Protein sim. GBank gi 2344830 emb CAA94727 - (Z70722) leucyl- tRNA synthase [Mycobacterium leprae]		UNCLASSIFIED	1029
7672	91254054 (15457, 15458)	Novel Protein sim. GBank gi 2369714 emb CAB09900 - (Z97178) elongation factor 2 [Beta vulgaris]		UNCLASSIFIED	1010
7673	11294033 (2077, 2078)	Novel Protein sim. GBank gi 2370478 emb CAB11506 - (Z98849) putative dna repair helicase [Schizosaccharomyces pombe]		UNCLASSIFIED	1022
7674	78990197 (13797, 13798)	Novel Protein sim. GBank gi 2384711 (AF013969) - antigen containing epitope to monoclonal antibody MMS-85/12 [Mus musculus]		UNCLASSIFIED	1003, 1008, 1017, 1044
7675	5825443 (13457, 13458)	Novel Protein sim. GBank gi 2384732 (AF015911) - NAC-1 protein [Rattus norvegicus]		UNCLASSIFIED	1058

7676	11686492 (19935, 19936)	Novel Protein sim. GBank gi 2388986 emb CAB11718 - (Z98980) actin associated protein [Schizosaccharomyces pombe]		UNCLASSIFIED	1004, 1031
7677	23333247 (5949, 5950)	Novel Protein sim. GBank gi 2392772 gb AAB70035.1 AAB7003 - (AC002534) putative chloroplast prephenate dehydratase [Arabidopsis thaliana]		UNCLASSIFIED	1053
7678	17672889 (22749, 22750)	Novel Protein sim. GBank gi 2408015 emb CAB16213.1 - (Z99162) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	1017
7679	11103035 (11249, 11250)	Novel Protein sim. GBank gi 2408224 (U93843) - HsdM [Klebsiella pneumoniae]		UNCLASSIFIED	1006, 1012
7680	20457009 (21863, 21864)	Novel Protein sim. GBank gi 2415399 (AF015775) - YodM [Bacillus subtilis]		UNCLASSIFIED	1010
7681	80076469 (1561, 1562)	Novel Protein sim. GBank gi 2429362 (AF020261) - proline rich protein [Santalum album]		UNCLASSIFIED	1034
7682	71047061 (22341, 22342)	Novel Protein sim. GBank gi 2429509 (AF025467) - contains similarity to drosophila DNA-binding protein K10 (NID:g8148) [Caenorhabditis elegans]		UNCLASSIFIED	1024
7683	36738341 (4193, 4194)	Novel Protein sim. GBank gi 2440104 emb CAB16677 - (Z99494) hypothetical protein MLCB57.37c [Mycobacterium leprae]		UNCLASSIFIED	1034
7684	65670184 (6729, 6730)	Novel Protein sim. GBank gi 2440127 emb CAB09984 - (Z97182) IpqO [Mycobacterium tuberculosis]		UNCLASSIFIED	1016
7685	87120503 (7739, 7740)	Novel Protein sim. GBank gi 2444165 (U91789) - Orf1 [Salmonella enteritidis]		UNCLASSIFIED	1025
7686	80079340 (5211, 5212)	Novel Protein sim. GBank gi 2467226 emb CAA63515 - (X92946) transposase [Lactococcus lactis]		UNCLASSIFIED	1034

7687	80216283 (19879, 19880)	Novel Protein sim. GBank gil2492823 sp Q12284 ERV2_YEAST - ERV2 PROTEIN PRECURSOR		UNCLASSIFIED	1003, 1004, 1006, 1008, 1010, 1022, 1024, 1026, 1031, 1034, 1039, 1044
7688	80027053 (13555, 13556)	Novel Protein sim. GBank gil2492825 sp Q53389 AMB2_BACST - N- CARBAMYL-L-AMINO ACID AMIDOHYDROLASE		UNCLASSIFIED	1006, 1016
7689	79867740 (12095, 12096)	Novel Protein sim. GBank gil2492900 sp Q04749 YMV8_YEAST - HYPOTHETICAL 47.1 KD PROTEIN IN NCA1- HMS1 INTERGENIC REGION		UNCLASSIFIED	1017
7690	32164246 (1585, 1586)	Novel Protein sim. GBank gil2492932 sp Q46805 YGEY_ECOLI - HYPOTHETICAL 44.8 KD PROTEIN IN KDUJ- LYSS INTERGENIC REGION		UNCLASSIFIED	1023
7691	21426257 (16551, 16552)	Novel Protein sim. GBank gil2492945 sp Q58201 ARLY_METJA - ARGININOSUCCINATE LYASE (ARGINOSUCCINASE) (ASAL)		UNCLASSIFIED	1022
7692	9126181 (4203, 4204)	Novel Protein sim. GBank gil2493550 sp Q02516 HAP5_YEAST - HAP5 TRANSCRIPTIONAL ACTIVATOR		UNCLASSIFIED	1006
7693	9383422 (5553, 5554)	Novel Protein sim. GBank gil2494679 sp Q08193 YOD0_YEAST - HYPOTHETICAL 51.9 KD PROTEIN IN MSE1- LAG2 INTERGENIC REGION PRECURSOR		UNCLASSIFIED	1017
7694	54994560 (11063, 11064)	Novel Protein sim. GBank gil2494700 sp P76535 YFEU_ECOLI - HYPOTHETICAL 31.2 KD PROTEIN IN CYP- AMIA INTERGENIC REGION		UNCLASSIFIED	1029
7695	70946830 (4571, 4572)	Novel Protein sim. GBank gil2494701 sp Q45582 YBBI_BACSU - HYPOTHETICAL 33.0 KD PROTEIN YBBI		UNCLASSIFIED	1029

7696	79859768 (19987, 19988)	Novel Protein sim. GBank gil2495497 sp P77489 YAGR_ECOLI - HYPOTHETICAL 78.1 KD PROTEIN IN INTF- EAEH INTERGENIC REGION		UNCLASSIFIED	1017
7697	29236487 (7323, 7324)	Novel Protein sim. GBank gil2495599 sp Q57184 YDAO_HAEIN - HYPOTHETICAL PROTEIN HI1371.1		UNCLASSIFIED	1026
7698	78980888 (7593, 7594)	Novel Protein sim. GBank gil2495673 sp Q57534 Y321_HAEIN - HYPOTHETICAL PROTEIN HI0321		UNCLASSIFIED	1016
7699	8900966 (14737, 14738)	Novel Protein sim. GBank gil2496353 sp P75419 Y259_MYCPN - HYPOTHETICAL PROTEIN MG259 HOMOLOG		UNCLASSIFIED	1004
7700	82454917 (12501, 12502)	Novel Protein sim. GBank gil2496481 sp Q50724 Y09S_MYCTU - HYPOTHETICAL 87.3 KD PROTEIN CY78.27C		UNCLASSIFIED	1001, 1012, 1022, 1023, 1027, 1031, 1039
7701	55281908 (17907, 17908)	Novel Protein sim. GBank gil2496536 sp Q50603 Y0DD_MYCTU - HYPOTHETICAL 24.0 KD PROTEIN CY1A11.13C		UNCLASSIFIED	1029, 1053
7702	30370138 (8293, 8294)	Novel Protein sim. GBank gil2496730 sp P55606 Y4OU_RHISN - HYPOTHETICAL PROTEIN Y4OU PRECURSOR		UNCLASSIFIED	1054
7703	10328691 (21887, 21888)	Novel Protein sim. GBank gil2496818 sp Q10940 YWS4_CAEEL - HYPOTHETICAL 13.1 KD PROTEIN B0310.4 IN CHROMOSOME X		UNCLASSIFIED	1025
7704	80020140 (4469, 4470)	Novel Protein sim. GBank gil2497069 sp Q03760 YMK7_YEAST - HYPOTHETICAL 45.2 KD PROTEIN IN ZDS2- URA5 INTERGENIC REGION		UNCLASSIFIED	1008, 1009, 1017, 1022
7705	79855876 (8573, 8574)	Novel Protein sim. GBank gil2497075 sp Q04511 YMI8_YEAST - HYPOTHETICAL 76.9 KD PROTEIN IN RPM2- TUB1 INTERGENIC REGION		UNCLASSIFIED	1017, 1022, 1044

7706	21433666 (337, 338)	Novel Protein sim. GBank gil2497110 sp Q04257 YMA3_YEAST - HYPOTHETICAL 34.0 KD PROTEIN IN GLO1- YPT7 INTERGENIC REGION		UNCLASSIFIED	1022
7707	17295003 (15097, 15098)	Novel Protein sim. GBank gil2497117 sp Q03690 IF31_YEAST - EUKARYOTIC TRANSLATION INITIATION FACTOR 3 ALPHA SUBUNIT (EIF-3 ALPHA) (EIF3 P135) (TRANSLATION INITIATION FACTOR EIF3, P135 SUBUNIT)		UNCLASSIFIED	1039
7708	80219823 (13803, 13804)	Novel Protein sim. GBank gil2497118 sp Q04347 YMP4_YEAST - HYPOTHETICAL 60.1 KD PROTEIN IN SEC59- ERG5 INTERGENIC REGION		UNCLASSIFIED	1003, 1006, 1022, 1034, 1044
7709	30623969 (14909, 14910)	Novel Protein sim. GBank gil2497121 sp Q04371 YMR7_YEAST - HYPOTHETICAL 54.1 KD PROTEIN IN PEX12- TAP42 INTERGENIC REGION		UNCLASSIFIED	1022, 1026
7710	80500344 (489, 490)	Novel Protein sim. GBank gil2497131 sp Q04659 YMT8_YEAST - HYPOTHETICAL 36.4 KD PROTEIN IN NUP116- FAR3 INTERGENIC REGION		UNCLASSIFIED	1006, 1010, 1012, 1034
7711	82460247 (15431, 15432)	Novel Protein sim. GBank gil2497136 sp Q04751 YMV9_YEAST - HYPOTHETICAL 32.3 KD PROTEIN IN NCA1- HMS1 INTERGENIC REGION		UNCLASSIFIED	1001, 1022, 1025
7712	80219097 (2931, 2932)	Novel Protein sim. GBank gil2497174 sp Q03218 YMA3_YEAST - HYPOTHETICAL 56.2 KD PROTEIN IN SIP18- SPT21 INTERGENIC REGION		UNCLASSIFIED	1001, 1022, 1025, 1034
7713	78799006 (4363, 4364)	Novel Protein sim. GBank gil2497176 sp Q03220 YMA5_YEAST - HYPOTHETICAL 37.0 KD PROTEIN IN SPT21- RGM1 INTERGENIC REGION		UNCLASSIFIED	1022

7714	39568538 (17349, 17350)	Novel Protein sim. GBank gi 2497179 sp Q12751 YM48_YEAST - HYPOTHETICAL 113.2 KD PROTEIN IN SSO2- HSC82 INTERGENIC REGION		UNCLASSIFIED	1006
7715	27955864 (18265, 18266)	Novel Protein sim. GBank gi 2497179 sp Q12751 YM48_YEAST - HYPOTHETICAL 113.2 KD PROTEIN IN SSO2- HSC82 INTERGENIC REGION		UNCLASSIFIED	1004, 1006, 1024, 1026
7716	27989945 (22367, 22368)	Novel Protein sim. GBank gi 2497208 sp Q04806 YM85_YEAST - HYPOTHETICAL 42.4 KD PROTEIN IN FAA4- HOR7 INTERGENIC REGION		UNCLASSIFIED	1016
7717	29024399 (16313, 16314)	Novel Protein sim. GBank gi 2497213 sp Q03508 YM8F_YEAST - HYPOTHETICAL 54.1 KD PROTEIN IN TPS3- IPP2 INTERGENIC REGION		UNCLASSIFIED	1017
7718	80501435 (9381, 9382)	Novel Protein sim. GBank gi 2497226 sp Q04889 YM94_YEAST - HYPOTHETICAL 38.2 KD PROTEIN IN PRE5- FET4 INTERGENIC REGION		UNCLASSIFIED	1012, 1025, 1039
7719	79115547 (6747, 6748)	Novel Protein sim. GBank gi 2497617 sp Q63313 LBP_RAT - LIPOPOLYSACCHARIDE-BINDING PROTEIN PRECURSOR (LBP)		UNCLASSIFIED	1003
7720	17927241 (7501, 7502)	Novel Protein sim. GBank gi 2497947 sp P74840 PRPD_SALTY - PRPD PROTEIN		UNCLASSIFIED	1038
7721	8490635 (3491, 3492)	Novel Protein sim. GBank gi 2497997 sp Q12175 MSH5_YEAST - MUTS PROTEIN HOMOLOG 5		UNCLASSIFIED	1024
7722	82125189 (20655, 20656)	Novel Protein sim. GBank gi 2498064 sp Q12746 YMM5_YEAST - HYPOTHETICAL 35.3 KD PROTEIN IN HMGS- TUB3 INTERGENIC REGION		UNCLASSIFIED	1006, 1008, 1016, 1022, 1023, 1024, 1034
7723	19738760 (1233, 1234)	Novel Protein sim. GBank gi 2498298 sp Q12387 DEC1_YEAST - DEC1 PROTEIN (MDM20 PROTEIN)		UNCLASSIFIED	1001

7724	25341197 (9125, 9126)	Novel Protein sim. GBank gij2498410 sp Q12315 GLE1_YEAST - RNA EXPORT FACTOR GLE1		UNCLASSIFIED	1009
7725	66694411 (4349, 4350)	Novel Protein sim. GBank gij2498414 sp Q48481 GLF8_KLEPN - PROBABLE UDP-GALACTOPYRANOSE MUTASE		UNCLASSIFIED	1009
7726	27837972 (4471, 4472)	Novel Protein sim. GBank gij2498438 sp Q12060 HF11_YEAST - TRANSCRIPTIONAL COACTIVATOR HF11/ADA1		UNCLASSIFIED	1006
7727	57299540 (7835, 7836)	Novel Protein sim. GBank gij2498477 sp Q06706 IKI3_YEAST - IKI3 PROTEIN		UNCLASSIFIED	1012, 1017, 1022, 1024, 1026, 1034
7728	86692192 (10737, 10738)	Novel Protein sim. GBank gij2498477 sp Q06706 IKI3_YEAST - IKI3 PROTEIN		UNCLASSIFIED	1018
7729	79176918 (12859, 12860)	Novel Protein sim. GBank gij2498788 sp Q61586 PLSB_MOUSE - GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT) (P90)		UNCLASSIFIED	1024
7730	11759311 (11471, 11472)	Novel Protein sim. GBank gij2498993 sp Q08314 TGT_HELPY - QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA - GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)		UNCLASSIFIED	1024
7731	78898837 (16583, 16584)	Novel Protein sim. GBank gij2499125 sp Q07878 VP13_YEAST - VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13		UNCLASSIFIED	1017
7732	79862148 (21471, 21472)	Novel Protein sim. GBank gij2499125 sp Q07878 VP13_YEAST - VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13		UNCLASSIFIED	1008, 1009, 1022, 1023, 1025, 1034, 1038, 1039

7733	78753190 (9101, 9102)	Novel Protein sim. GBank gil2499128 sp Q12194 YP66_YEAST - HYPOTHETICAL 54.9 KD PROTEIN IN VPS28- BTS1 INTERGENIC REGION		UNCLASSIFIED	1008, 1044
7734	17292485 (11409, 11410)	Novel Protein sim. GBank gil2499481 sp Q49092 YBL3_MORCA - HYPOTHETICAL 46.4 KD PROTEIN IN BLOR-1 3'REGION (ORF3)		UNCLASSIFIED	1039
7735	8490481 (3581, 3582)	Novel Protein sim. GBank gil2499966 sp Q41228 PSE1_NICSY - PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E A)		UNCLASSIFIED	1034
7736	80071069 (10247, 10248)	Novel Protein sim. GBank gil2501040 sp Q05814 SYP_MYCTU - PROLYL- TRNA SYNTHETASE (PROLINE--TRNA LIGASE) (PRORS)		UNCLASSIFIED	1010, 1031
7737	79116389 (21605, 21606)	Novel Protein sim. GBank gil2501167 sp P71353 YHGF_HAEIN - HYPOTHETICAL PROTEIN H10568		UNCLASSIFIED	1013
7738	79569002 (17669, 17670)	Novel Protein sim. GBank gil2501514 sp Q64324 STX2_MOUSE - SYNTAXIN BINDING PROTEIN 2 (UNC-18 HOMOLOG 2) (UNC-18B) (MUSEC1)		UNCLASSIFIED	1004
7739	27974545 (5775, 5776)	Novel Protein sim. GBank gil2501571 sp Q02891 YP95_YEAST - HYPOTHETICAL 51.7 KD PROTEIN IN SEC82- MSY1 INTERGENIC REGION		UNCLASSIFIED	1004
7740	66727316 (20067, 20068)	Novel Protein sim. GBank gil2501583 sp Q55156 Y064_SYNY3 - HYPOTHETICAL 43.0 KD PROTEIN SLR0064		UNCLASSIFIED	1049
7741	19515814 (17869, 17870)	Novel Protein sim. GBank gil2501593 sp Q57951 Y531_METJA - HYPOTHETICAL PROTEIN MJ0531		UNCLASSIFIED	1024

7742	39434881 (6483, 6484)	Novel Protein sim. GBank gij2501738 sp Q06639 YD03_YEAST - PUTATIVE 101.7 KD TRANSCRIPTIONAL REGULATORY PROTEIN IN PRO1-CPR5 INTERGENIC REGION		UNCLASSIFIED	1010, 1024
7743	66397374 (6619, 6620)	Novel Protein sim. GBank gij2506132 sp P36683 ACO2_ECOLI - ACONITATE HYDRATASE 2 (CITRATE HYDROLYASE 2) (ACONITASE 2)		UNCLASSIFIED	1008
7744	91235299 (18345, 18346)	Novel Protein sim. GBank gij2506139 sp P49661 COPD_ORYSA - COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN)		UNCLASSIFIED	1003
7745	80021107 (1979, 1980)	Novel Protein sim. GBank gij2506393 sp P31576 FIXX_ECOLI - FERREDOXIN LIKE PROTEIN		UNCLASSIFIED	1024
7746	17939502 (15333, 15334)	Novel Protein sim. GBank gij2506465 sp P39811 GLR2_ECOLI - GLUTAREDOXIN 2 (GRX2)		UNCLASSIFIED	1039
7747	79640300 (2399, 2400)	Novel Protein sim. GBank gij2506493 sp P38036 YGCB_ECOLI - HYPOTHETICAL 100.5 KD PROTEIN IN IAP-CYSH INTERGENIC REGION		UNCLASSIFIED	1039
7748	80054815 (13895, 13896)	Novel Protein sim. GBank gij2506625 sp P52697 YBHE_ECOLI - HYPOTHETICAL 36.3 KD PROTEIN IN MODG-BIOA INTERGENIC REGION		UNCLASSIFIED	1022
7749	25315630 (63, 64)	Novel Protein sim. GBank gij2506765 sp P47029 YJ14_YEAST - HYPOTHETICAL 117.2 KD PROTEIN IN EXO70-ARP4 INTERGENIC REGION		UNCLASSIFIED	1009
7750	88064332 (10935, 10936)	Novel Protein sim. GBank gij2506915 sp P21769 ODFP_RAT - OUTER DENSE FIBER PROTEIN (RT7 PROTEIN) (RTS 5/1)		UNCLASSIFIED	1008, 1017

7751	79612632 (138, 140)	Novel Protein sim. GBank gil2506975 sp P15272 AMN_ECOLI - AMP NUCLEOSIDASE		UNCLASSIFIED	1022
7752	46899493 (22217, 22218)	Novel Protein sim. GBank gil2506985 sp P50851 CC4H_HUMAN - CDC4- LIKE PROTEIN		UNCLASSIFIED	1040
7753	79429507 (9707, 9708)	Novel Protein sim. GBank gil2507147 sp P22257 TIG_ECOLI - TRIGGER FACTOR (TF)		UNCLASSIFIED	1017
7754	20727860 (13309, 13310)	Novel Protein sim. GBank gil2507295 sp P39199 YFCB_ECOLI - HYPOTHETICAL ADENINE-SPECIFIC METHYLASE IN AROC-FADL INTERGENIC REGION		UNCLASSIFIED	1006
7755	79452313 (17921, 17922)	Novel Protein sim. GBank gil2507347 sp P04050 RPB1_YEAST - DNA- DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (B220)		UNCLASSIFIED	1010, 1024
7756	80500925 (20841, 20842)	Novel Protein sim. GBank gil2507511 sp P37340 YDHE_ECOLI - HYPOTHETICAL 49.4 KD PROTEIN IN RIBC- PYKF INTERGENIC REGION		UNCLASSIFIED	1012
7757	80223858 (1479, 1480)	Novel Protein sim. GBank gil253435 bbs 110869 - (S42186) Vps35p [Saccharomyces cerevisiae=yeast, Peptide, 937 aa] [Saccharomyces cerevisiae]		UNCLASSIFIED	1003, 1004, 1006, 1009, 1022, 1024
7758	8486607 (14063, 14064)	Novel Protein sim. GBank gil2559004 (AF026269) - prominin [Mus musculus]		UNCLASSIFIED	1022
7759	66370567 (19587, 19588)	Novel Protein sim. GBank gil2578444 emb CAA47812 - (X67427) ptbA [Pisum sativum]		UNCLASSIFIED	1054
7760	79963875 (17209, 17210)	Novel Protein sim. GBank gil2580435 dbj BAA23140 - (D76414) N- acetylmutamoyl-L-alanine amidase [Staphylococcus aureus]		UNCLASSIFIED	1022

7761	11131459 (5193, 5194)	Novel Protein sim. GBank gi 2612821 emb CAA04438 - (AJ000978) cis/trans isomerase [Pseudomonas putida]		UNCLASSIFIED	1024
7762	24137026 (22867, 22868)	Novel Protein sim. GBank gi 2612821 emb CAA04438 - (AJ000978) cis/trans isomerase [Pseudomonas putida]		UNCLASSIFIED	1003
7763	78184018 (8411, 8412)	Novel Protein sim. GBank gi 2619000 (AF027868) - YoaT [Bacillus subtilis]		UNCLASSIFIED	1053
7764	16280147 (11715, 11716)	Novel Protein sim. GBank gi 2621084 (AE000797) - conserved protein [Methanobacterium thermoautotrophicum]		UNCLASSIFIED	1054
7765	80071744 (19397, 19398)	Novel Protein sim. GBank gi 2622039 (AE000888) - type I restriction modification system, subunit S [Methanobacterium thermoautotrophicum]		UNCLASSIFIED	1022, 1026
7766	57306083 (1373, 1374)	Novel Protein sim. GBank gi 2622565 (AE000906) - unknown [Methanobacterium thermoautotrophicum]		UNCLASSIFIED	1008, 1029
7767	46741764 (7493, 7494)	Novel Protein sim. GBank gi 2632006 emb CAA05565 - (AJ002571) YkaA [Bacillus subtilis]		UNCLASSIFIED	1054
7768	79628516 (3083, 3084)	Novel Protein sim. GBank gi 2632009 emb CAA05568 - (AJ002571) YkcB [Bacillus subtilis]		UNCLASSIFIED	1039
7769	78677252 (13097, 13098)	Novel Protein sim. GBank gi 2632162 emb CAA04544 - (AJ001118) monoglyceride lipase [Mus musculus]		UNCLASSIFIED	1022
7770	85818137 (1141, 1142)	Novel Protein sim. GBank gi 2632362 emb CAB11871 - (Z99104) similar to hypothetical proteins [Bacillus subtilis]		UNCLASSIFIED	1019
7771	46660015 (5991, 5992)	Novel Protein sim. GBank gi 2633555 emb CAB13058 - (Z99110) similar to fructose phosphotransferase system enzyme II [Bacillus subtilis]		UNCLASSIFIED	1029

7772	30194801 (19993, 19994)	Novel Protein sim. GBank gij2633555[emb]CAB13058] - (Z99110) similar to fructose phosphotransferase system enzyme II [Bacillus subtilis]		UNCLASSIFIED	1026
7773	20456631 (16819, 16820)	Novel Protein sim. GBank gij2633811[emb]CAB13313] - (Z99111) phosphotransferase system (PTS) fructose-specific enzyme IIBC component [Bacillus subtilis]		UNCLASSIFIED	1010
7774	79478222 (3845, 3846)	Novel Protein sim. GBank gij2634069[emb]CAB13570] - (Z99112) similar to hypothetical proteins [Bacillus subtilis]		UNCLASSIFIED	1038
7775	23331942 (10069, 10070)	Novel Protein sim. GBank gij2642157 (AC003000) - ankyrin-like protein [Arabidopsis thaliana]		UNCLASSIFIED	1029
7776	65903327 (11607, 11608)	Novel Protein sim. GBank gij2645205 (U63648) - p160 myb-binding protein [Mus musculus]		UNCLASSIFIED	1022, 1023
7777	28992723 (20547, 20548)	Novel Protein sim. GBank gij2649977 (AE001060) - conserved hypothetical protein [Archaeoglobus fulgidus]		UNCLASSIFIED	1044
7778	78917042 (15245, 15246)	Novel Protein sim. GBank gij2650410 (AE001090) - glutamine ABC transporter, periplasmic glutamine-binding protein (ginH) [Archaeoglobus fulgidus]		UNCLASSIFIED	1039
7779	80250210 (18941, 18942)	Novel Protein sim. GBank gij2650749 (AE001114) - A. fulgidus predicted coding region AF2347 [Archaeoglobus fulgidus]		UNCLASSIFIED	1006
7780	86474147 (12887, 12888)	Novel Protein sim. GBank gij2661856[emb]CAB06301] - (Z83933) protoporphyrin IX Mg chelatase encoding subunit of 144 kDa [Chlorobium vibrioforme]		UNCLASSIFIED	1026, 1029
7781	65686309 (6079, 6080)	Novel Protein sim. GBank gij2662165[dbj]BAA23714] - (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]		UNCLASSIFIED	1024, 1031

7782	66644385 (6219, 6220)	Novel Protein sim. GBank gij2662165 dbj BAA23714 - (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]		UNCLASSIFIED	1038
7783	56002941 (13563, 13564)	Novel Protein sim. GBank gij266346 sp Q01292 ILV5 SPIOL - KETOL-ACID REDUCTOISOMERASE PRECURSOR (ACETOHYDROXY-ACID REDUCTOISOMERASE) (ALPHA-KETO-BETA- HYDROXYLACIL REDUCTOISOMERASE)		UNCLASSIFIED	1003
7784	78955542 (15773, 15774)	Novel Protein sim. GBank gij266859 sp Q01329 PTA1_YEAST - PTA1 PROTEIN		UNCLASSIFIED	1039
7785	65451776 (19467, 19468)	Novel Protein sim. GBank gij266859 sp Q01329 PTA1_YEAST - PTA1 PROTEIN		UNCLASSIFIED	1016
7786	78736132 (18201, 18202)	Novel Protein sim. GBank gij2673912 (AC002561) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	1003, 1017
7787	10067356 (949, 950)	Novel Protein sim. GBank gij267439 sp P11288 YAAA_ECOLI - HYPOTHETICAL 29.6 KD PROTEIN IN THRC- TALB INTERGENIC REGION		UNCLASSIFIED	1044
7788	28780390 (20403, 20404)	Novel Protein sim. GBank gij267497 sp P30267 YKAA_BACFI - HYPOTHETICAL 50.9 KD PROTEIN IN KATA 3'REGION (ORF A)		UNCLASSIFIED	1022
7789	80047436 (1239, 1240)	Novel Protein sim. GBank gij2688556 (AE001164) - vacuolar X-prolyl dipeptidyl aminopeptidase I (pepX) [Borrelia burgdorferi]		UNCLASSIFIED	1004, 1034
7790	20369375 (7893, 7894)	Novel Protein sim. GBank gij2695820 emb CAA15890 - (AL021006) hypothetical protein Rv1234 [Mycobacterium tuberculosis]		UNCLASSIFIED	1004

7791	30407879 (15065, 15066)	Novel Protein sim. GBank gi 2695954 emb CAA15847 - (AL010186) hypothetical protein Rv1170 [Mycobacterium tuberculosis]		UNCLASSIFIED	1026
7792	11094040 (18347, 18348)	Novel Protein sim. GBank gi 2708667 (AF037441) - putative 19.5 kDa protein [Edwardsiella ictaluri]		UNCLASSIFIED	1022
7793	20428302 (21037, 21038)	Novel Protein sim. GBank gi 2738164 (U91842) - hypothetical protein [Bacillus firmus]		UNCLASSIFIED	1010
7794	20456914 (15561, 15562)	Novel Protein sim. GBank gi 2760909 (AF036925) - family 10 xylanase [Caldicellulosiruptor sp. R169B.1]		UNCLASSIFIED	1010
7795	11695905 (12909, 12910)	Novel Protein sim. GBank gi 2764825 emb CAA66092 - (X97452) paaC [Escherichia coli]		UNCLASSIFIED	1034
7796	20751341 (585, 586)	Novel Protein sim. GBank gi 2765047 emb CAA71110 - (Y09990) putative RNaseE homologue [Salmonella typhi]		UNCLASSIFIED	1053
7797	11684107 (10331, 10332)	Novel Protein sim. GBank gi 2766551 (AF040104) - polysaccharide export protein [Rhizobium leguminosarum bv. trifolii]		UNCLASSIFIED	1016
7798	8910955 (11753, 11754)	Novel Protein sim. GBank gi 2772619 (U93355) - hypothetical 32.1 kDa protein [Erwinia herbicola]		UNCLASSIFIED	1017
7799	78460104 (13233, 13234)	Novel Protein sim. GBank gi 2791420 emb CAA16014.1 - (AL021185) lppS [Mycobacterium tuberculosis]		UNCLASSIFIED	1026
7800	54817140 (5215, 5216)	Novel Protein sim. GBank gi 2791495 emb CAA16032 - (AL021246) hypothetical protein Rv2455c [Mycobacterium tuberculosis]		UNCLASSIFIED	1029
7801	11695477 (13129, 13130)	Novel Protein sim. GBank gi 2791510 emb CAA16047 - (AL021246) glbO [Mycobacterium tuberculosis]		UNCLASSIFIED	1034

7802	51628181 (16371, 16372)	Novel Protein sim. GBank gij2791635 emb CAA16122.1 - (AL021287) hypothetical protein Rv3037c [Mycobacterium tuberculosis]	UNCLASSIFIED	1040
7803	65460236 (239, 240)	Novel Protein sim. GBank gij2791917 emb CAA73543 - (Y13095) ORF142 [Staphylococcus sciuri]	UNCLASSIFIED	1016
7804	80079357 (7451, 7452)	Novel Protein sim. GBank gij2804624 (U89347) - malonate decarboxylase gamma subunit [Acinetobacter calcoaceticus]	UNCLASSIFIED	1034
7805	20729449 (19857, 19858)	Novel Protein sim. GBank gij2811044 sp O06250 Y115_MYCTU - HYPOTHETICAL 46.9 KD PROTEIN CY77.05C	UNCLASSIFIED	1006
7806	78466439 (2219, 2220)	Novel Protein sim. GBank gij2815604 (AF025438) - Opa-interacting protein OIP2 [Homo sapiens]	UNCLASSIFIED	1026
7807	80021193 (14907, 14908)	Novel Protein sim. GBank gij2826874 emb CAA76168 - (Y16311) Spo0J-like protein [Streptomyces coelicolor]	UNCLASSIFIED	1006, 1022, 1024, 1039
7808	78460855 (15407, 15408)	Novel Protein sim. GBank gij2828292 emb CAA16706.1 - (AL021687) neoxanthin cleavage enzyme-like protein [Arabidopsis thaliana]	UNCLASSIFIED	1044
7809	65472844 (11551, 11552)	Novel Protein sim. GBank gij2829501 sp P71550 YT14_MYCTU - HYPOTHETICAL 13.9 KD PROTEIN CY10D7.14C	UNCLASSIFIED	1023
7810	82060965 (4467, 4468)	Novel Protein sim. GBank gij2829815 sp P95095 CSTA_MYCTU - CARBON STARVATION PROTEIN A HOMOLOG	UNCLASSIFIED	1004, 1006, 1010, 1012, 1016, 1024
7811	33764003 (19789, 19790)	Novel Protein sim. GBank gij2829890 (AC002396) - Hypothetical protein [Arabidopsis thaliana]	UNCLASSIFIED	1026

7812	29444855 (11263, 11264)	Novel Protein sim. GBank gjl2829910 (AC002291) - Unknown protein, contains regulator of chromosome condensation motifs [Arabidopsis thaliana]	UNCLASSIFIED	1026
7813	87892765 (15689, 15690)	Novel Protein sim. GBank gjl282994 pir S27762 - Sip1 protein - barley	UNCLASSIFIED	1025
7814	65855363 (3851, 3852)	Novel Protein sim. GBank gjl2833221 sp Q12214 HOS1_YEAST - HOS1 PROTEIN	UNCLASSIFIED	1003, 1006, 1022, 1024
7815	78455768 (12259, 12260)	Novel Protein sim. GBank gjl2833225 sp Q12499 NOP5_YEAST - NUCLEOLAR PROTEIN NOP5	UNCLASSIFIED	1026
7816	80381812 (18483, 18484)	Novel Protein sim. GBank gjl2833311 sp Q21828 YNFD_CAEEL - HYPOTHETICAL 18.9 KD PROTEIN R07E5.13 IN CHROMOSOME III	UNCLASSIFIED	1029
7817	79776510 (5085, 5086)	Novel Protein sim. GBank gjl283920 pir S27939 - tensin - chicken	UNCLASSIFIED	1008, 1025, 1030, 1050
7818	11077819 (5599, 5600)	Novel Protein sim. GBank gjl283920 pir S27939 - tensin - chicken	UNCLASSIFIED	1024
7819	80243856 (9737, 9738)	Novel Protein sim. GBank gjl283920 pir S27939 - tensin - chicken	UNCLASSIFIED	1001, 1004, 1022, 1024
7820	20447603 (4607, 4608)	Novel Protein sim. GBank gjl2842445 emb CAA11813 - (AJ224072) histone 1 [Mytilus edulis]	UNCLASSIFIED	1024
7821	10219102 (11817, 11818)	Novel Protein sim. GBank gjl284775 pir S27870 - house-keeping protein - mouse	UNCLASSIFIED	1004
7822	32303167 (1089, 1090)	Novel Protein sim. GBank gjl2852636 (AF007155) - unknown [Homo sapiens]	UNCLASSIFIED	1029
7823	8490182 (10035, 10036)	Novel Protein sim. GBank gjl285303 pir A42261 - heparan sulfate proteoglycan - rat	UNCLASSIFIED	1024
7824	66002613 (2897, 2898)	Novel Protein sim. GBank gjl2853599 (AF031898) - CheZ [Pseudomonas putida]	UNCLASSIFIED	1003, 1010

7825	80222147 (4409, 4410)	Novel Protein sim. GBank gil2854158 gb AAC02577.1 - (AF045641) No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	1006, 1009, 1022
7826	28389737 (15949, 15950)	Novel Protein sim. GBank gil285953 dbj BAA03498 - (D14664) KIAA0022 [Homo sapiens]		UNCLASSIFIED	1003, 1044
7827	32723325 (14967, 14968)	Novel Protein sim. GBank gil288590 emb CAA48159.1 - (X68020) ARP [Saccharomyces cerevisiae]		UNCLASSIFIED	1001
7828	21661213 (14079, 14080)	Novel Protein sim. GBank gil2894206 emb CAA17072 - (AL021840) hypothetical protein Rv3258c [Mycobacterium tuberculosis]		UNCLASSIFIED	1024
7829	91226994 (4187, 4188)	Novel Protein sim. GBank gil2894612 emb CAA17146 - (AL021889) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	1010
7830	9945895 (7063, 7064)	Novel Protein sim. GBank gil2894795 (U76907) - 17 kDa common-antigen [Rickettsia sp.]		UNCLASSIFIED	1044
7831	20286920 (12301, 12302)	Novel Protein sim. GBank gil2896719 emb CAA17198.1 - (AL021897) hypothetical protein Rv1082 [Mycobacterium tuberculosis]		UNCLASSIFIED	1034
7832	79430083 (5869, 5870)	Novel Protein sim. GBank gil290497 (L10328) - f562 [Escherichia coli]		UNCLASSIFIED	1017
7833	77523099 (22081, 22082)	Novel Protein sim. GBank gil2909643 emb CAA17455 - (AL021942) hypothetical protein Rv0584 [Mycobacterium tuberculosis]		UNCLASSIFIED	1023
7834	86473942 (14193, 14194)	Novel Protein sim. GBank gil2911072 emb CAA17534.1 - (AL021960) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	1054
7835	65704798 (6615, 6616)	Novel Protein sim. GBank gil2916881 emb CAA17829.1 - (AL022004) hypothetical protein Rv0823c [Mycobacterium tuberculosis]		UNCLASSIFIED	1023
7836	47656865 (2111, 2112)	Novel Protein sim. GBank gil2920641 (AF044503) - hcp [Escherichia coli]		UNCLASSIFIED	1029

7837	25266008 (17317, 17318)	Novel Protein sim. GBank gi 2921422 (AF036677) - unknown [Salmonella typhimurium]	UNCLASSIFIED	1054
7838	8911583 (5195, 5196)	Novel Protein sim. GBank gi 2924463(emb) CAA17703 - (AL022021) hypothetical protein Rv1781c [Mycobacterium tuberculosis]	UNCLASSIFIED	1003
7839	24138405 (10129, 10130)	Novel Protein sim. GBank gi 2947228 (AF031886) - erythrocyte binding protein [Plasmodium yoelii yoelii]	UNCLASSIFIED	1003
7840	30003865 (19331, 19332)	Novel Protein sim. GBank gi 2952522 (AF051357) - golgin-245 [Mus musculus]	UNCLASSIFIED	1016, 1022
7841	79627101 (12111, 12112)	Novel Protein sim. GBank gi 2952527(emb) AAC05772.1 - (AF051356) putative hemolysin [Streptococcus mutans]	UNCLASSIFIED	1001
7842	29691795 (19947, 19948)	Novel Protein sim. GBank gi 2952528(emb) AAC05773.1 - (AF051356) pyruvate-formate lyase activating enzyme [Streptococcus mutans]	UNCLASSIFIED	1024
7843	78788387 (3031, 3032)	Novel Protein sim. GBank gi 295616 (M24378) - IRA1 [Saccharomyces cerevisiae]	UNCLASSIFIED	1022
7844	70451483 (13197, 13198)	Novel Protein sim. GBank gi 2956769(emb) CAA17882.1 - (AL022103) phosphatidylinositol phosphate phosphatase; synaptotagmin-like [Schizosaccharomyces pombe]	UNCLASSIFIED	1049
7845	94939107 (2045, 2046)	Novel Protein sim. GBank gi 2960107(emb) CAA18005.1 - (AL022121) hypothetical protein Rv3683 [Mycobacterium tuberculosis]	UNCLASSIFIED	1012
7846	80183435 (12791, 12792)	Novel Protein sim. GBank gi 2970646 (AF051945) - Xin [Mus musculus]	UNCLASSIFIED	1001, 1022
7847	80084754 (13053, 13054)	Novel Protein sim. GBank gi 2970646 (AF051945) - Xin [Mus musculus]	UNCLASSIFIED	1001
7848	10159775 (16073, 16074)	Novel Protein sim. GBank gi 2970646 (AF051945) - Xin [Mus musculus]	UNCLASSIFIED	1001

7849	29346130 (9281, 9282)	Novel Protein sim. GBank gil2980781[emb]CAA18208.1] - (AL022198) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	1022
7850	79820669 (5125, 5126)	Novel Protein sim. GBank gil2981631[dbj]BAA25253.1] - (AB012223) ORF2 [Canis familiaris]		UNCLASSIFIED	1039
7851	24135395 (6119, 6120)	Novel Protein sim. GBank gil2981631[dbj]BAA25253.1] - (AB012223) ORF2 [Canis familiaris]		UNCLASSIFIED	1003
7852	29265223 (6879, 6880)	Novel Protein sim. GBank gil2981631[dbj]BAA25253.1] - (AB012223) ORF2 [Canis familiaris]		UNCLASSIFIED	1022
7853	86678455 (9117, 9118)	Novel Protein sim. GBank gil2981631[dbj]BAA25253.1] - (AB012223) ORF2 [Canis familiaris]		UNCLASSIFIED	1007
7854	6626611 (21651, 21652)	Novel Protein sim. GBank gil2981631[dbj]BAA25253.1] - (AB012223) ORF2 [Canis familiaris]		UNCLASSIFIED	1022
7855	66489048 (22713, 22714)	Novel Protein sim. GBank gil2981631[dbj]BAA25253.1] - (AB012223) ORF2 [Canis familiaris]		UNCLASSIFIED	1029
7856	86694804 (525, 526)	Novel Protein sim. GBank gil2983010 (AE000684) - glutamate racemase [Aquifex aeolicus]		UNCLASSIFIED	1018
7857	80502803 (8839, 8840)	Novel Protein sim. GBank gil2983039 (AE000686) - proline-tRNA synthetase [Aquifex aeolicus]		UNCLASSIFIED	1012
7858	78472450 (19866, 19866)	Novel Protein sim. GBank gil2983116 (AE000690) - hypothetical protein [Aquifex aeolicus]		UNCLASSIFIED	1044
7859	78784143 (843, 844)	Novel Protein sim. GBank gil2983213 (AE000697) - mannose-6-phosphate isomerase/mannose-1-phosphate guanyl transferase [Aquifex aeolicus]		UNCLASSIFIED	1006, 1022, 1031
7860	85523012 (16153, 16154)	Novel Protein sim. GBank gil2983357 (AE000708) - pantothenate metabolism flavoprotein [Aquifex aeolicus]		UNCLASSIFIED	1049

7861	65707960 (8035, 8036)	Novel Protein sim. GBank gjl2984222 (AE000766) - fucose-1-phosphate aldolase [Aquifex aeolicus]		UNCLASSIFIED	1023
7862	80249025 (8811, 8812)	Novel Protein sim. GBank gjl2995312[emb CAA18340] - (AL022268) hypothetical protein SC4H2.25 [Streptomyces coelicolor]		UNCLASSIFIED	1003, 1004, 1006, 1010
7863	20458553 (17827, 17828)	Novel Protein sim. GBank gjl2995352[emb CAA04606.1] - (AJ001206) pep1 [Streptomyces coelicolor]		UNCLASSIFIED	1010
7864	20474031 (137, 138)	Novel Protein sim. GBank gjl2996650 (AC004493) - KIAA0324 [Homo sapiens]		UNCLASSIFIED	1004, 1010
7865	25328221 (22311, 22312)	Novel Protein sim. GBank gjl2997593 (AF020816) - glucose-6-phosphate/phosphate-translocator precursor [Solanum tuberosum]		UNCLASSIFIED	1008
7866	87466974 (9189, 9190)	Novel Protein sim. GBank gjl3023275[sp Q43763 AGLU_HORVU - ALPHA-GLUCOSIDASE PRECURSOR (MALTASE)]		UNCLASSIFIED	1025
7867	39384799 (11597, 11598)	Novel Protein sim. GBank gjl3023717[sp Q08649 ESA1_YEAST - ESA1 PROTEIN]		UNCLASSIFIED	1034
7868	20288062 (18607, 18608)	Novel Protein sim. GBank gjl3024872[sp Q55790 Y074_SYNY3 - HYPOTHETICAL 52.8 KD PROTEIN SLR0074]		UNCLASSIFIED	1034
7869	19746688 (9269, 9270)	Novel Protein sim. GBank gjl3025061[sp P75949 YCF0_ECOLI - HYPOTHETICAL 37.6 KD PROTEIN IN FHUE-NDH INTERGENIC REGION]		UNCLASSIFIED	1039
7870	79842574 (10157, 10158)	Novel Protein sim. GBank gjl3025094[sp Q03835 YD98_YEAST - HYPOTHETICAL 32.5 KD PROTEIN IN MSH6-BMH2 INTERGENIC REGION]		UNCLASSIFIED	1003, 1008, 1017, 1039
7871	79833832 (21747, 21748)	Novel Protein sim. GBank gjl3025094[sp Q03835 YD98_YEAST - HYPOTHETICAL 32.5 KD PROTEIN IN MSH6-BMH2 INTERGENIC REGION]		UNCLASSIFIED	1003, 1008, 1017

7872	8491792 (22965, 22966)	Novel Protein sim. GBank gil3025215[sp]Q18486[YLC4 CAEEL - HYPOTHETICAL 81.0 KD PROTEIN C35D10.4 IN CHROMOSOME III]		UNCLASSIFIED	1022
7873	25328743 (21973, 21974)	Novel Protein sim. GBank gil3025282[sp]P71691[YR40_MYCTU - HYPOTHETICAL 35.8 KD PROTEIN CY21B4.40]		UNCLASSIFIED	1008
7874	34080752 (2149, 2150)	Novel Protein sim. GBank gil3043548[dbj]BAA25438] - (AB011084) KIAA0512 protein [Homo sapiens]		UNCLASSIFIED	1000
7875	86473919 (9041, 9042)	Novel Protein sim. GBank gil3047114 (AF058919) - No definition line found [Arabidopsis thaliana]		UNCLASSIFIED	1054
7876	86678808 (22677, 22678)	Novel Protein sim. GBank gil304931 (L17086) - putative [Escherichia coli]		UNCLASSIFIED	1007
7877	37034876 (9545, 9546)	Novel Protein sim. GBank gil3063877[emb]CAA18562] - (AL022486) putative integral membrane protein [Mycobacterium leprae]		UNCLASSIFIED	1012
7878	10054330 (20143, 20144)	Novel Protein sim. GBank gil3080473[emb]CAA18668] - (AL022602) udp-n- acetylglucosamine-n-acetylmuramyl - (pentapeptide) pyrophosphoryl-undecaprenol n- acetylglucosamine transferase [Mycobacterium leprae]		UNCLASSIFIED	1012
7879	77967677 (20237, 20238)	Novel Protein sim. GBank gil3080500[emb]CAA18697] - (AL022602) hypothetical protein MLCB288.31c [Mycobacterium leprae]		UNCLASSIFIED	1036
7880	66043054 (5827, 5828)	Novel Protein sim. GBank gil3080530[emb]CAA18658] - (AL022600) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	1016
7881	17898362 (13573, 13574)	Novel Protein sim. GBank gil3080767 (AF041381) - putative transcriptional repressor E2F-6 [Homo sapiens]		UNCLASSIFIED	1044

7882	17884279 (15611, 15612)	Novel Protein sim. GBank gij3114661 (AF061267) - putative alpha-ketoglutarate-dependent hypophosphite dioxygenase [Pseudomonas stutzeri]		UNCLASSIFIED	1039
7883	78406525 (4977, 4978)	Novel Protein sim. GBank gij3122314 sp Q34971 KDPD_RATRA - SENSOR PROTEIN KDPD		UNCLASSIFIED	1016
7884	79864487 (18177, 18178)	Novel Protein sim. GBank gij3122404 sp Q06225 MURC_MYCTU - UDP-N-ACETYL-MURAMATE--ALANINE LIGASE (UDP-N-ACETYL-MURANOYL-L-ALANINE SYNTHETASE)		UNCLASSIFIED	1012
7885	78380245 (9285, 9286)	Novel Protein sim. GBank gij3122905 sp Q26687 SYM_METTH - METHIONYL-TRNA SYNTHETASE (METHIONINE--TRNA LIGASE) (METRS)		UNCLASSIFIED	1000, 1008, 1026, 1029
7886	11291349 (16705, 16706)	Novel Protein sim. GBank gij3122969 sp Q63679 TSGA_RAT - TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA)		UNCLASSIFIED	1022
7887	27964611 (13209, 13210)	Novel Protein sim. GBank gij3122982 sp Q12093 TRMU_YEAST - PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE		UNCLASSIFIED	1008, 1034
7888	20436829 (14787, 14788)	Novel Protein sim. GBank gij3123014 sp P87498 VIT1_CHICK - VITELLOGENIN I PRECURSOR (MINOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LV1); PHOSVITIN (PV); LIPOVITELLIN II (LV2)]; YGP421		UNCLASSIFIED	1010
7889	80061727 (6313, 6314)	Novel Protein sim. GBank gij3123021 sp Q90508 VIT1_FUNHE - VITELLOGENIN I PRECURSOR (VTG I) [CONTAINS: LIPOVITELLIN 1 (LV1); PHOSVITIN (PV); LIPOVITELLIN 2 (LV2)]		UNCLASSIFIED	1024

7890	80243196 (9995, 9996)	Novel Protein sim. GBank gij3123034[spIQ15011]Y025_HUMAN - HYPOTHETICAL PROTEIN KIAA0025		UNCLASSIFIED	1001, 1004, 1009, 1022, 1024, 1044
7891	78768175 (15041, 15042)	Novel Protein sim. GBank gij3123209[spIP25039]EFG1_YEAST - ELONGATION FACTOR G, MITOCHONDRIAL 1 PRECURSOR (MEF-G-1)		UNCLASSIFIED	1017, 1022
7892	32302888 (22125, 22126)	Novel Protein sim. GBank gij3128208 (AC004077) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	1029
7893	78920553 (15195, 15196)	Novel Protein sim. GBank gij3128218 (AC004077) - putative end13 protein [Arabidopsis thaliana]		UNCLASSIFIED	1039
7894	97981207 (4473, 4474)	Novel Protein sim. GBank gij3128374 (AF010496) - hypothetical protein [Rhodobacter capsulatus]		UNCLASSIFIED	1031
7895	37805818 (13351, 13352)	Novel Protein sim. GBank gij3128382 (AF013282) - MmTbx14 [Mus musculus]		UNCLASSIFIED	1058
7896	57280237 (18163, 18164)	Novel Protein sim. GBank gij3135267 (AC003058) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	1034
7897	20708130 (17915, 17916)	Novel Protein sim. GBank gij3142214[dbjBAA28327] - (AB010150) mannosyltransferase [Escherichia coli]		UNCLASSIFIED	1053
7898	27996632 (3525, 3526)	Novel Protein sim. GBank gij3142291 (AC002411) - Contains similarity to adenylate cyclase gb AF012921 from Magnaporthe griseae. EST gb Z24512 comes from this gene. [Arabidopsis thaliana]		UNCLASSIFIED	1030
7899	19881159 (1045, 1046)	Novel Protein sim. GBank gij3153821 (AF062655) - plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]		UNCLASSIFIED	1034
7900	86477499 (15339, 15340)	Novel Protein sim. GBank gij3153821 (AF062655) - plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]		UNCLASSIFIED	1029

7901	82401801 (3917, 3918)	Novel Protein sim. GBank gil3169721 gb AAC17939.1 - (AF007569) Gstr [Bradyrhizobium japonicum]		UNCLASSIFIED	1001, 1038
7902	78073994 (16735, 16736)	Novel Protein sim. GBank gil3170887 (AF061555) - ubiquitin-protein ligase E3-alpha [Mus musculus]		UNCLASSIFIED	1024
7903	78675661 (9921, 9922)	Novel Protein sim. GBank gil3183285 sp P77649 YDIU_ECOLI - HYPOTHETICAL 54.4 KD PROTEIN IN AROH- NLPC INTERGENIC REGION		UNCLASSIFIED	1022
7904	27973628 (19483, 19484)	Novel Protein sim. GBank gil3183285 sp P77649 YDIU_ECOLI - HYPOTHETICAL 54.4 KD PROTEIN IN AROH- NLPC INTERGENIC REGION		UNCLASSIFIED	1053
7905	80023962 (561, 562)	Novel Protein sim. GBank gil3183438 sp P77774 YFGL_ECOLI - HYPOTHETICAL 41.9 KD PROTEIN IN XSEA- HISS INTERGENIC REGION		UNCLASSIFIED	1053
7906	20467859 (9553, 9554)	Novel Protein sim. GBank gil3183489 sp Q06489 YP18_YEAST - HYPOTHETICAL 45.0 KD PROTEIN IN PIS1- CLB2 INTERGENIC REGION		UNCLASSIFIED	1010
7907	17868673 (3007, 3008)	Novel Protein sim. GBank gil3184082 emb CAA19338 - (AL023781) N- terminal acetyltransferase 1 [Schizosaccharomyces pombe]		UNCLASSIFIED	1024
7908	27966043 (5589, 5590)	Novel Protein sim. GBank gil3191996 emb CAA19395 - (AL023787) hypothetical protein SC2E1.20 [Streptomyces coelicolor]		UNCLASSIFIED	1006
7909	56149085 (9999, 10000)	Novel Protein sim. GBank gil3193284 (AF069298) - No definition line found [Arabidopsis thaliana]		UNCLASSIFIED	1003
7910	11399346 (21849, 21850)	Novel Protein sim. GBank gil3193327 (AF069299) - No definition line found [Arabidopsis thaliana]		UNCLASSIFIED	1006

7911	11769816 (19519, 19520)	Novel Protein sim. GBank gjl3212996 gb AAC23433.1 - (AC004997) match to ESTs Z43979 (NID:g573097), R19699 (NID:g774333), T59198 (NID:g661035), and AA027979 (NID:g1494038) [Homo sapiens]		UNCLASSIFIED	1016
7912	38861267 (15877, 15878)	Novel Protein sim. GBank gjl322752 pir A44226 - auxin-independent growth promoter - Nicotiana tabacum		UNCLASSIFIED	1026
7913	80019495 (421, 422)	Novel Protein sim. GBank gjl3242702 (AC003040) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	1006, 1023, 1024, 1034
7914	14994658 (3651, 3652)	Novel Protein sim. GBank gjl3242702 (AC003040) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	1027
7915	57514736 (11335, 11336)	Novel Protein sim. GBank gjl3242705 (AC003040) - putative nicotinate phosphoribosyltransferase [Arabidopsis thaliana]		UNCLASSIFIED	1001, 1006, 1009, 1024, 1026
7916	39559043 (15043, 15044)	Novel Protein sim. GBank gjl3256023 emb CAA17228.1 - (AL021897) hypothetical protein Rv1112 [Mycobacterium tuberculosis]		UNCLASSIFIED	1008
7917	87466650 (17647, 17648)	Novel Protein sim. GBank gjl3256605 dbj BAA29288.1 - (AP000001) 125aa long hypothetical protein [Pyrococcus horikoshii]		UNCLASSIFIED	1015
7918	82375773 (14609, 14610)	Novel Protein sim. GBank gjl3256606 dbj BAA29289.1 - (AP000001) 171aa long hypothetical protein [Pyrococcus horikoshii]		UNCLASSIFIED	1001, 1006
7919	19424875 (12551, 12552)	Novel Protein sim. GBank gjl3256608 dbj BAA29291.1 - (AP000001) 235aa long hypothetical protein [Pyrococcus horikoshii]		UNCLASSIFIED	1054

7920	78919297 (15079, 15080)	Novel Protein sim. GBank gi 3256779 dbj BAA29462 - (AP000002) 422aa long hypothetical protein [Pyrococcus horikoshii]		UNCLASSIFIED	1008
7921	79554658 (18475, 18476)	Novel Protein sim. GBank gi 3257120 dbj BAA29803 - (AP000003) 230aa long hypothetical protein [Pyrococcus horikoshii]		UNCLASSIFIED	1039
7922	79810415 (5301, 5302)	Novel Protein sim. GBank gi 3258173 dbj BAA30856.1 - (AP000007) 306aa long hypothetical UDP-glucose 4-epimerase [Pyrococcus horikoshii]		UNCLASSIFIED	1008
7923	11809488 (10017, 10018)	Novel Protein sim. GBank gi 3261489 emb CAA15488 - (AL008687) speE [Mycobacterium tuberculosis]		UNCLASSIFIED	1022
7924	87899077 (21423, 21424)	Novel Protein sim. GBank gi 3261523 emb CAA17328 - (AL021928) mmpl3 [Mycobacterium tuberculosis]		UNCLASSIFIED	1015
7925	38916141 (14009, 14010)	Novel Protein sim. GBank gi 3281846 emb CAA07004 - (AJ006404) late elongated hypocotyl [Arabidopsis thaliana]		UNCLASSIFIED	1026
7926	79815120 (6489, 6500)	Novel Protein sim. GBank gi 3282044 emb CAA74300 - (Y13967) alpha- aminoadipate reductase large subunit [Penicillium chrysogenum]		UNCLASSIFIED	1044
7927	35933503 (15729, 15730)	Novel Protein sim. GBank gi 3282331 (AF012100) - GalR-LacI homolog; PtxS [Pseudomonas aeruginosa]		UNCLASSIFIED	1053
7928	55660774 (18057, 18058)	Novel Protein sim. GBank gi 3287876 sp P72349 NDAD_ALCXX - D- AMINOACYLASE (N-ACYL-D-AMINO-ACID DEACYLASE)		UNCLASSIFIED	1041
7929	12902105 (16365, 16366)	Novel Protein sim. GBank gi 3292814 emb CAA19804.1 - (AL031018) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	1031, 1050
7930	79844169 (18589, 18590)	Novel Protein sim. GBank gi 3294467 (U89341) - phosphoglucosyltransferase 1 [Zea mays]		UNCLASSIFIED	1017, 1022, 1026, 1039